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OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:15 ; Search time 221.345 Seconds
(without alignments)
311.909 Million cell updates/sec

Title: US-10-530-253-13
Sequence: 1 MFQDPQRPRKLPQLCTELQ.....WTGRKMSCCRSRRRTETQL 151

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 8:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	828	99.8	248	8	AD044062 Amino aci
2	828	99.8	248	8	AD044064 Amino aci
3	826	99.5	151	6	AA022640 HPV-16 pr
4	826	99.5	151	6	AA022636 HPV prote
5	826	99.5	151	8	AD044072 Amino aci
6	826	99.5	162	8	AAW35742 Human pap
7	826	99.5	248	8	AD044060 Amino aci
8	823	99.2	151	8	ADU66364 Human pap
9	823	99.2	158	2	AA022766 HPV E6 pe
10	823	99.2	158	3	AAV82462 Human pap
11	823	99.2	158	4	AA022640 HPV-16 pr
12	823	99.2	158	7	AD044072 Amino aci
13	823	99.2	158	7	AD044060 Amino aci
14	823	99.2	158	8	ADU66364 Human pap
15	823	99.2	158	9	AA022766 HPV E6 pe
16	823	99.2	158	9	AAV82462 Human pap
17	823	99.2	158	9	AA022640 HPV-16 pr
18	823	99.2	158	9	AA022636 HPV prote
19	823	99.2	158	9	AA022640 HPV-16 pr
20	823	99.2	158	9	AA022636 HPV prote
21	823	99.2	158	9	AA022640 HPV-16 pr
22	823	99.2	158	9	AA022636 HPV prote
23	823	99.2	158	9	AA022640 HPV-16 pr

24	823	99.2	248	8	AD044070 Amino aci
25	823	99.2	256	8	ADR47005 Human pap
26	823	99.2	256	10	AEF40157 Human pap
27	823	99.2	263	2	AA022725 HPV 16 E6
28	823	99.2	266	2	AA022725 HPV 16 E6
29	823	99.2	273	2	AA022725 HPV 16 E6
30	823	99.2	273	2	AA022725 HPV 16 E6
31	823	99.2	273	2	AA022725 HPV 16 E6
32	823	99.2	292	2	AA022725 HPV 16 E6
33	823	99.2	292	2	AA022725 HPV 16 E6
34	823	99.2	292	2	AA022725 HPV 16 E6
35	823	99.2	371	2	AA022725 HPV 16 E6
36	823	99.2	371	2	AA022725 HPV 16 E6
37	823	99.2	371	2	AA022725 HPV 16 E6
38	823	99.2	390	2	AA022725 HPV 16 E6
39	823	99.2	390	2	AA022725 HPV 16 E6
40	823	99.2	390	2	AA022725 HPV 16 E6
41	821	98.9	248	8	AD044066 Amino aci
42	818	98.6	151	3	AAV57808 HPV-16 E6
43	815	98.2	158	8	ADL90078 Human pap
44	779.5	93.9	243	2	AAW99369 Papilloma
45	580	69.9	149	2	AA040919 HPV E6 re

ALIGNMENTS

RESULT 1	AD044062	AD044062 standard; protein; 248 AA.
ID	AD044062	
XX	AD044062	
AC	AD044062	
XX	AD044062	
DT	15-JUL-2004	(first entry)
DE	Amino acid sequence of a fusion protein designated E6E7TeM.	
XX		
KM	E6 protein; E7 protein; fusion protein; HPV16, HPV-associated cancer;	
KW	cervical cancer; immune response; lower gastrointestinal tract cancer;	
KW	anal cancer; reproductive system cancer; penile cancer; vulvar cancer.	
OS	Human papillomavirus type 16.	
XX	Synthetic.	
FN	WO2004030636-A2.	
PD	15-APR-2004.	
XX		
PF	02-OCT-2003; 2003US-0415929P.	
XX		
FR	03-OCT-2002; 2002US-0415929P.	
XX		
PA	(AMHP) WYETH HOLDINGS CORP.	
XX		
PI	Smith L, Cassetti MC;	
XX		
DR	WPI; 2004-316328/29.	
XX	N-PSDB; AD044063.	
PT	New polypeptide comprising human papillomavirus E6 and E7 polypeptides,	
PT	useful for treating or preventing human papillomavirus (HPV)-associated	
PT	cancers, e.g. cervical cancer.	
XX		
PS	Claim 22; Page 68-69; 101pp; English.	
XX		
CC	The present sequence represents a fusion protein, comprising E6 and E7	
CC	polypeptides from human papillomavirus type 16 (HPV16). The fusion	
CC	protein is designated E6E7TeM, and comprises an E6 amino terminus (where	
CC	residues 63 and 106 have been replaced with glycine) and an E7 carboxy	
CC	terminus (where residues 24 and 26 have been replaced with glycine).	
CC	E6E7TeM is representative of fusion proteins of the invention. The	
CC	specification describes human papillomavirus E6 and E7 polypeptides,	
CC	where the E7 polypeptide has mutations at any one or more of the amino	

CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC there sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 99.8%; Score 828; DB 8; Length 248;

Best Local Similarity 98.7%; Pred. No. 4.6e-84; Mismatches 149; Conservative 0; Indels 2; Gaps 0;

QY 1 MFQDPQRRPKLPQLCTELQTTIHDIIECYCKQQLRREYDFAFRLDCTVYRDGMPY 60
DB 1 MFQDPQRRPKLPQLCTELQTTIHDIIECYCKQQLRREYDFAFRLDCTVYRDGMPY 60
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLBOQYNNKPLCDLLIRCIHXKPLCPBEKQRHLD 120
DB 61 AVGDCKLKFYSKISEYRHYCYSVYGTTLBOQYNNKPLCDLLIRCIHXKPLCPBEKQRHLD 120
QY 121 KQRFHNIRGRWTRGCMSCCRSSRTRETQL 151
DB 121 KQRFHNIRGRWTRGCMSCCRSSRTRETQL 151

RESULT 2

ADO44064 ADO44064 standard; protein; 248 AA.

XX ADO44064;

DT 15-JUL-2004 (first entry)

XX Amino acid sequence of a fusion protein designated E6E7PentM.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
XX cervical cancer; immune response; lower gastrointestinal tract cancer;
XX anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

OS Human papillomavirus type 16.
XX Synthetic.

XX WO2004030636-A2.

XX 15-APR-2004.

XX 02-OCT-2003; 2003WO-US031726.

XX 03-OCT-2002; 2002US-0415929P.

XX (AMHP) WYETH HOLDINGS CORP.

XX Smith L, Caesetti MC;

XX WPI; 2004-316328/29.

XX N-PSDB; ADO44065.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

PS Claim 22; Page 70-71; 101pp; English.

XX The present sequence represents a fusion protein, comprising E6 and E7
XX polypeptides from human papillomavirus type 16 (HPV16). The fusion
XX protein is designated E6E7PentM, and comprises an E6 amino terminus
XX (where residues 63 and 106 have been replaced with glycine) and an E7
XX carboxy terminus (where residues 24, 26 and 91 have been replaced with

CC glycine). E6E7PentM is representative of fusion proteins of the
CC invention. The specification describes human papillomavirus E6 and E7
CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of there sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 99.8%; Score 828; DB 8; Length 248;

Best Local Similarity 98.7%; Pred. No. 4.6e-84; Mismatches 149; Conservative 0; Indels 2; Gaps 0;

QY 1 MFQDPQRRPKLPQLCTELQTTIHDIIECYCKQQLRREYDFAFRLDCTVYRDGMPY 60
DB 1 MFQDPQRRPKLPQLCTELQTTIHDIIECYCKQQLRREYDFAFRLDCTVYRDGMPY 60
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTTLBOQYNNKPLCDLLIRCIHXKPLCPBEKQRHLD 120
DB 61 AVGDCKLKFYSKISEYRHYCYSVYGTTLBOQYNNKPLCDLLIRCIHXKPLCPBEKQRHLD 120
QY 121 KQRFHNIRGRWTRGCMSCCRSSRTRETQL 151
DB 121 KQRFHNIRGRWTRGCMSCCRSSRTRETQL 151

RESULT 3

AAO22640 AAO22640 standard; protein; 151 AA.

XX AAO22640;

DT 15-MAY-2003 (first entry)

XX HPV-16 protein sequence, SEQ ID NO 27.

XX Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;
XX cancer; human papilloma virus; cervix; cell-mediated immune response;
XX HPV; HPV-16.

XX Human papilloma virus.

XX WO2003008649-A1.

XX 30-JAN-2003.

XX 19-JUL-2002; 2002WO-US023198.

XX 20-JUL-2001; 2001US-0306809P.

XX (TEXA) UNIV TEXAS SYSTEM.

XX Sastry KJ, Tortolero-Luna G, Follen M;

XX WPI; 2003-239363/23.

PT Determining a possible recurrence of a (pre-)cancerous growth in a
PT patient infected with human papilloma virus (HPV), comprises incubating
PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
PT immune response.

PS Disclosure; Page 129-130; 132pp; English.

XX The invention relates to a novel method for determining the possibility
XX of recurrence of a (pre-)cancerous growth in a patient infected with
XX human papilloma virus (HPV) or suspected of being infected with HPV, and

CC has or had a (pre-)cancerous growth on or around the cervix. The novel
CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
CC the patient, and assaying the sample for a cell-mediated immune response
CC against the peptide. The method is useful for determining the possibility
CC and preventing the recurrence of a (pre-)cancerous growth in a patient
CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
CC E7 peptides are useful in immunotherapy for the preventing or reducing
CC the risk of development of (pre-)cancerous growths. This sequence
CC represents an HPV-16 protein of the invention

SQ Sequence 151 AA;

Query Match 99.5%; Score 826; DB 6; Length 151;

Best Local Similarity 98.7%; Pred. No. 4.2e-84; Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCLVYDGNPY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCLVYDGNPY 60
QY 61 AVXDKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLRCINXQKPLCEEKQRHLD 120
DB 61 AVXDKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLRCINXQKPLCEEKQRHLD 120
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 4

AAO22636 ID AAO22636 standard; protein; 151 AA.

AC AAO22636;

DT 15-MAY-2003 (first entry)

DE HPV protein sequence, SEQ ID No 20.

XX Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth;
KW cancer; human papilloma virus; cervix; cell-mediated immune response;
KW HPV; HPV-16.

OS Human papilloma virus.

WO2003008649-A1.

PD 30-JAN-2003.

PF 19-JUL-2002; 2002WO-US023198.

PR 20-JUL-2001; 2001US-0306809P.

PA (TEXA) UNIV TEXAS SYSTEM.

PI Sastiy KJ, Tortolero-Luna G, Follen M;

WP1; 2003-239363/23.

PT Determining a possible recurrence of a (pre-)cancerous growth in a
PT patient infected with human papilloma virus (HPV), comprises incubating
PT the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
PT immune response.

PS Disclosure; Page 125-126; 132pp; English.

CC The invention relates to a novel method for determining the possibility
CC of recurrence of a (pre-)cancerous growth in a patient infected with
CC human papilloma virus (HPV) or suspected of being infected with HPV, and
CC has or had a (pre-)cancerous growth on or around the cervix. The novel
CC method comprises incubating an E6 or E7 peptide of HPV with a sample from
CC the patient, and assaying the sample for a cell-mediated immune response
CC against the peptide. The method is useful for determining the possibility

CC and preventing the recurrence of a (pre-)cancerous growth in a patient
CC infected with HPV or suspected of being infected with HPV. The HPV E6 or
CC E7 peptides are useful in immunotherapy for the preventing or reducing
CC the risk of development of (pre-)cancerous growths. This sequence
CC represents an HPV protein of the invention

SQ Sequence 151 AA;

Query Match 99.5%; Score 826; DB 6; Length 151;

Best Local Similarity 98.7%; Pred. No. 4.2e-84; Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCLVYDGNPY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYVCKQQLRREYDPAFRLDCLVYDGNPY 60
QY 61 AVXDKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLRCINXQKPLCEEKQRHLD 120
DB 61 AVXDKLKFYSKISERYHYCYSVYGTLEQYNNKPLCDLLRCINXQKPLCEEKQRHLD 120
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 5

ADO44072 ID ADO44072 standard; protein; 151 AA.

AC ADO44072;

DT 15-JUL-2004 (first entry)

DE Amino acid sequence of a wild type HPV16 E6 protein.

XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KW cervical cancer; immune response; lower gastrointestinal tract cancer;
KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.

OS Human papillomavirus type 16.

WO2004030636-A2.

PD 15-APR-2004.

PF 02-OCT-2003; 2003WO-US031726.

PR 03-OCT-2002; 2002US-0415929P.

PA (AMHP) WYETH HOLDINGS CORP.

PI Smith L, Caesetti MC;

WP1; 2004-316326/29.

PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.

PS Claim 1; Page 76-77; 101pp; English.

CC The present sequence represents a wild type E6 protein from human
CC papillomavirus type 16 (HPV16), which is used to produce fusion proteins
CC of the invention. The specification describes human papillomavirus E6 and
CC E7 polypeptides, where the E7 polypeptide has mutations at any one or
CC more of the amino acid corresponding to amino acids 24, 26 or 91 of the
CC sequence given in ADO44072 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating

immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.

Sequence 151 AA:

Query Match Best Local Similarity 99.5%; Score 826; DB 8; Length 151;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREYDFAFDLCIVYRDGNPY 60

1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREYDFAFDLCIVYRDGNPY 60

61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQYKNRPLCDLLIRCIHXKQPLCPPEEKQRHLD 120

61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQYKNRPLCDLLIRCIHXKQPLCPPEEKQRHLD 120

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

at position 350 is associated with an increased risk of developing cervical dysplasia or cervical cancer; and (2) preparing a cervical sample to expose any HPV-16 E6 protein in the sample and determining if the amino acid at position 83 of the protein (see position 90 in AAW35742 and AAW35742 for comparison) is Val or Leu, where the presence of Val at position 83 that is associated with an increased risk of developing cervical dysplasia or cervical cancer. The present sequence represents the variant protein sequence for HPV-16 E6. The 350G variant correlates well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:14 for negative Pap scores; 4:2 for CIN I; 1:6 for CIN II; 2:9 for CIN III; 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 162 AA:

Query Match Best Local Similarity 99.5%; Score 826; DB 2; Length 162;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREYDFAFDLCIVYRDGNPY 60

1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREYDFAFDLCIVYRDGNPY 60

61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQYKNRPLCDLLIRCIHXKQPLCPPEEKQRHLD 120

61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQYKNRPLCDLLIRCIHXKQPLCPPEEKQRHLD 120

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

at position 350 is associated with an increased risk of developing cervical dysplasia or cervical cancer; and (2) preparing a cervical sample to expose any HPV-16 E6 protein in the sample and determining if the amino acid at position 83 of the protein (see position 90 in AAW35742 and AAW35742 for comparison) is Val or Leu, where the presence of Val at position 83 that is associated with an increased risk of developing cervical dysplasia or cervical cancer. The present sequence represents the variant protein sequence for HPV-16 E6. The 350G variant correlates well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:14 for negative Pap scores; 4:2 for CIN I; 1:6 for CIN II; 2:9 for CIN III; 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 162 AA:

Query Match Best Local Similarity 99.5%; Score 826; DB 2; Length 162;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREYDFAFDLCIVYRDGNPY 60

1 MFQDPQERPRKLPQCTELQTTIHDIIECYCKQQLRREYDFAFDLCIVYRDGNPY 60

61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQYKNRPLCDLLIRCIHXKQPLCPPEEKQRHLD 120

61 AVXDKCLKFYSKISEYHRYCYSVYGTLEQYKNRPLCDLLIRCIHXKQPLCPPEEKQRHLD 120

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

121 KQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of
 CC the sequence given in ADO44072. The polypeptides of the invention are
 CC useful for treating or preventing human papillomavirus (HPV)-associated
 CC cancer, such as cervical cancer. The fusion proteins and nucleic acids
 CC encoding the fusion proteins are useful for generating immune responses
 CC against HPV. They are also useful for treating lower gastrointestinal
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
 CC system, including penile and vulvar cancer.

XX Sequence 248 AA;

Query Match 99.5%; Score 826; DB 8; Length 248;
 Best Local Similarity 98.7%; Pred. No. 7.7e-84;
 Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGPNY 60
 DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGPNY 60
 QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
 DB 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
 DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 8

ID ADO66364 standard; protein, 151 AA.

XX ADU66364;

DT 10-FEB-2005 (first entry)

XX Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 5.

XX vaccine; MHC class I pathway; antigen specific immune response; tumor;

KM E7 protein; E6 protein.

XX Human papillomavirus type 16.

PN WO2004098526-A2.

PD 18-NOV-2004.

PF 05-MAY-2004; 2004WO-US013756.

PR 05-MAY-2003; 2003US-0467602P.

PA (UYJO) UNIV JOHNS HOPKINS.

PI Wu T, Hung CF;

XX WPI; 2004-813972/80.

PT New nucleic acid molecules encoding a fusion polypeptide comprising an
 PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine
 PT for inducing or enhancing immune response or for inhibiting or preventing
 PT tumor growth.

XX Disclosure; SEQ ID NO 5; 67bp; English.

XX The invention comprises a nucleic acid molecule (DNA vaccine) that
 CC encodes a fusion polypeptide which is useful as a vaccine composition.
 CC The nucleic acid of the invention contains: a first nucleic acid encoding
 CC a polypeptide that promotes processing via the MHC class I pathway; a
 CC second sequence encoding a signal peptide; and a third sequence encoding
 CC an antigenic polypeptide. The DNA vaccine of the invention is useful for
 CC inducing or enhancing an antigen specific immune response, or to inhibit

CC growth or prevent re-growth of a tumor expressing Human papillomavirus
 CC (HPV) E7 or E6 protein. The present amino acid sequence represents a
 CC human papillomavirus type 16 (HPV16) E6 protein of the invention.

XX Sequence 151 AA;

Query Match 99.2%; Score 823; DB 8; Length 151;
 Best Local Similarity 98.0%; Pred. No. 9.2e-84;
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGPNY 60
 DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYDPAFADLCIVRDGPNY 60
 QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
 DB 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQYNNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
 QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
 DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 9

ID AAR22766 standard; peptide, 158 AA.

XX AAR22766;

DT 25-MAR-2003 (revised)

DT 21-SEP-1992 (first entry)

XX HPV E6 peptide.

XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.

XX Synthetic.

OS Homo sapiens.

PN WO9205248-A.

PD 02-APR-1992.

XX 26-SEP-1991; 91WO-US007081.

XX 26-SEP-1990; 90US-00588384.

PA (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;

XX WPI; 1992-132119/16.

PT Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
 PT recombinant cells encoding them, useful in treatment and prophylaxis of
 PT cervical warts or cancer resulting from HPV infection.

XX Disclosure; Fig 7; 81bp; English.

XX The peptide is the sequence of the human papillomavirus HPV 16 E6
 CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
 CC of HPV 16 E6 were synthesized by standard Merrifield synthesis. Examples
 CC of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions
 CC contg. these peptides, antibodies against the peptides, or recombinant
 CC cells contg. the gene encoding the immuno- genic peptides may be utilised
 CC in methods for inhibiting and treating HPV infection and tumour
 CC initiation and progression e.g. in the prevention or retardation of
 CC cervical warts and cervical carcinoma resulting from HPV infection. See
 CC also AAR22767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 25-MAR-2003 to correct PI field.)

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPGCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGMPY 60
DB 8 MFODPQERPRKLPGCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGMPY 67

QY 61 AVXDCKLKFYSKISEYHNYCYSVGTTLBQOYNKPLCDLLIRCIHXKPLCPBEKQRLHD 120
DB 68 AVCDCKLKFYSKISEYHNYCYSLVGTTLBQOYNKPLCDLLIRCIHXKPLCPBEKQRLHD 127

QY 121 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 151
DB 128 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 158

RESULT 10
AAY82462
ID AAY82462 standard; protein; 158 AA.
XX
AC AAY82462;
XX
DT 30-JUN-2000 (first entry)
XX
DE Human papillomavirus E6 protein containing two zinc finger motifs.
XX
KM Chelated zinc finger; therapeutic; treatment; prophylaxis; HPV;
KW mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;
KW wart.
XX
OS Human papillomavirus.
XX
FH Key Location/Qualifiers
FT Misc-difference 37..73
FT /note= "forms a zinc finger motif"
FT Misc-difference 110..146
FT /note= "forms a zinc finger motif"
XX
PN WO200014063-A1.
XX
PD 16-MAR-2000.
XX
PF 03-SEP-1999; 99WO-AU000724.
XX
PR 04-SEP-1998; 98AU-00005733.
PR 15-JUL-1999; 99AU-00001645.
XX
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (HUGH/) HUGHES E J L.
XX
PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;
XX
DR WPI; 2000-256917/22.
XX
PT Polyulfide and dithionodisulfide agents, useful for the treatment or
PT prophylaxis of diseases caused by mammalian papillomavirus, are
PT disruptors of a chelated metal cation domain in an HPV gene encoded
PT protein.
XX
PS Disclosure; Fig 1; 78pp; English.
XX
CC The present invention describes an agent used in the treatment or
CC prophylaxis of a disease caused or exacerbated by HPV (mammalian
CC papillomavirus) comprising a compound capable of reducing, inhibiting or
CC otherwise decreasing the activity of a protein encoded by an HPV gene by
CC facilitating disruption of a chelated metal cation domain present in the
CC protein. An agent of the present invention can be used to treat cervical
CC cancer or its HPV associated precursor lesions or other HPV associated
CC cancers and/or warts. The present sequence represents a human
CC papillomavirus E6 protein containing two zinc finger motifs, as given in
CC the exemplification of the present invention
XX

SQ Sequence 158 AA:
Query Match 99.2%; Score 823; DB 3; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPGCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGMPY 60
DB 8 MFODPQERPRKLPGCTELQTTIHDIIECYCKQQLLRREYDFAFRDLCTIVRDGMPY 67

QY 61 AVXDCKLKFYSKISEYHNYCYSVGTTLBQOYNKPLCDLLIRCIHXKPLCPBEKQRLHD 120
DB 68 AVCDCKLKFYSKISEYHNYCYSLVGTTLBQOYNKPLCDLLIRCIHXKPLCPBEKQRLHD 127

QY 121 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 151
DB 128 KKQRFHNIRGRWTCRCMSCRSSRTRRETOL 158

RESULT 11
AAB98420
ID AAB98420 standard; protein; 158 AA.
XX
AC AAB98420;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human papillomavirus protein HPV16 E6.
XX
KM Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;
KW epitope; T cell; identification; vaccine; infection; genital wart;
KW neoplastic growth; antiviral.
XX
OS Human papillomavirus.
XX
FH WO200141799-A1.
XX
PN 14-JUN-2001.
XX
PD 11-DEC-2000; 2000WO-US033549.
XX
PF 10-DEC-1999; 99US-0172705P.
PR 15-AUG-2000; 2000US-00641528.
XX
PA (EPIM-) EPIMMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;
XX
DR WPI; 2001-381497/40.
XX
PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for
PT treating HPV infections.
XX
PS Disclosure; Page 20-21; 756pp; English.
XX
CC The present invention describes an isolated prepared human papillomavirus
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine
CC production. Peptides and corresponding nucleic acid compositions from the
CC present invention are useful for stimulating an immune response to HPV by
CC stimulating the production of CTL or HTL responses, specifically in the
CC treatment or prophylaxis of HPV infection, in persons who have not
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides
CC can also be used in a tetramer staining assay to assess peripheral blood
CC mononuclear cells for the presence of antigen-specific CTLs following
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune
CC recall responses or evaluate the efficacy of a vaccine. The vaccine
CC compositions are useful for removing warts or treating HPV infections.
CC The epitopes for inclusion in an epitope-base vaccine may be selected
CC from conserved regions of viral or tumour-associated antigens, which
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes
CC that may be present in whole antigens can be avoided with the use of
CC epitope-base vaccines. An additional advantage is the ability to combine
CC selected epitopes (CTL and HTL) and to modify the composition of the

CC epitopes achieving enhanced immunogenicity, the major benefit of the
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent
CC polypeptide sequences used in the exemplification of the present
CC invention

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 4; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGPNY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGPNY 67
QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLRCINXQKPLCPBEKQRHLD 120
DB 68 AVCDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLRCINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 12
ADP09515
ID ADP09515 standard; protein; 158 AA.

XX ADF09515;

DT 12-FEB-2004 (first entry)

DE Human papillomavirus 16 E6 SEQ ID NO:16.

XX human; protein-protein interaction; virucide; cytostatic; vaccine;
KM human papilloma virus; HPV; cancer.

XX Human papillomavirus.

OS WO2003068940-A2.

XX 21-AUG-2003.

PF 14-FEB-2003; 2003WO-US004594.

XX 14-FEB-2002; 2002US-0356911P.

XX (CURA-) CURAGEN CORP.

PA (HOFF) HOFFMANN LA ROCHE INC.

PI Jackson A, Ooi CE, Lewin DA, Cuthill S;

XX WPI; 2003-689668/65.

DR N-PSDB; ADF09607.

PT New purified complex comprising a first polypeptide and a second
PT polypeptide, useful for identifying agents for treating/preventing a
PT condition involving altered level of the complex e.g. human papilloma
PT virus infection, or cancer.

XX Example 3; SEQ ID NO 16; 156pp; English.

XX The invention relates to a novel purified complex comprising a first
CC polypeptide and a second polypeptide, where the polypeptides comprise
CC defined amino acid sequences listed in the specification, and where the
CC first polypeptide binds to the second polypeptide. A complex of the
CC invention has virucide and cytostatic activity and may have a use as a
CC vaccine. The complex is useful for identifying agents for treating or
CC preventing a conditions involving altered level of the complex, e.g.
CC human papilloma virus (HPV) infection, or cancer. The compositions,
CC antibodies, vectors and methods are useful for treating such diseases.
CC The sequences shown in ADF09500-ADP09583 represent proteins of the
CC invention.

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 7; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGPNY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAPFDLCIVRDGPNY 67
QY 61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLRCINXQKPLCPBEKQRHLD 120
DB 68 AVCDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLRCINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 13
ADU66363
ID ADU66363 standard; protein; 158 AA.

XX ADU66363;

DT 10-FEB-2005 (first entry)

DE Human papillomavirus type 16 (HPV16) E6 protein - SEQ ID 4.

XX vaccine; MHC class I pathway; antigen specific immune response; tumor;
KM E7 protein; E6 protein.

XX Human papillomavirus type 16.

OS WO2004098526-A2.

XX 18-NOV-2004.

PF 05-MAY-2004; 2004WO-US013756.

XX 05-MAY-2003; 2003US-0467602P.

XX (UYJO) UNIV JOHNS HOPKINS.

PI Wu T, Hung CF;

XX WPI; 2004-813972/80.

PT New nucleic acid molecules encoding a fusion polypeptide comprising an
PT antigen, a signal peptide, and a heat shock protein, useful as a vaccine
PT for inducing or enhancing immune response or for inhibiting or preventing
PT tumor growth.

XX Claim 11; SEQ ID NO 4; 67pp; English.

XX The invention comprises a nucleic acid molecule (DNA vaccine) that
CC encodes a fusion polypeptide which is useful as a vaccine composition.
CC The nucleic acid of the invention contains: a first nucleic acid encoding
CC a polypeptide that promotes processing via the MHC class I pathway; a
CC second sequence encoding a signal peptide; and a third sequence encoding
CC an antigenic polypeptide. The DNA vaccine of the invention is useful for
CC inducing or enhancing an antigen specific immune response, or to inhibit
CC growth or prevent re-growth of a tumor expressing Human papillomavirus
CC (HPV) E7 or E6 protein. The present amino acid sequence represents a
CC human papillomavirus type 16 (HPV16) E6 protein of the invention.

XX Sequence 158 AA;

Query Match 99.2%; Score 823; DB 8; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCCKQQLLRREYDFAFRDLCTIVYRDGNPY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIILECYCCKQQLLRREYDFAFRDLCTIVYRDGNPY 67
QY 61 AVXDKCLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLIRCIINXQKPLCPREEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHYCYSLVGTTLQOYNKPLCDLIRCIINXQKPLCPREEKQRHLD 127
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 14
AEA40817 standard; protein; 158 AA.
XX AEA40817;
XX AEA40817;
XX 28-JUL-2005 (first entry)
DE Anti-apoptotic vector HPV E6 antigenic protein, SEQ ID 7.
XX immunogenicity; immunogenicity-potentiating polypeptide; IPP; T-cell;
KM vaccine; immune stimulation; tumor; cytostatic.
XX Human papillomavirus - 16.
XX WO2005047501-A1.
XX 26-MAY-2005.
XX 24-FEB-2004; 2004WO-US005292.
XX 24-FEB-2003; 2003US-0449429P.
PR 18-JUL-2003; 2003US-048827P.
PR 31-DEC-2003; 2003US-0533792P.
XX (UYJO) UNIV JOHNS HOPKINS.
XX Wu T, Hung CF, Kim T;
PI WPI; 2005-367009/37.
DR GENBANK; NC_001526.
PT New nucleic acid composition comprising a first nucleic acid vector
PT encoding an antigenic polypeptide and a second nucleic acid vector
PT inhibiting the growth of a tumor.
XX
PS Disclosure; SEQ ID NO 7; 158bp; English.
XX The invention relates to a novel nucleic acid composition useful as an
CC immunogen. The composition comprises a combination of: a first nucleic
CC acid vector comprising a first sequence encoding an antigenic polypeptide
CC or peptide, and optionally, a second sequence encoding a first
CC sequence and encoding an immunogenicity-potentiating polypeptide (IPP);
CC and a second nucleic acid vector encoding an anti-apoptotic polypeptide.
CC When the second vector is administered with the first vector to a
CC subject, a T cell mediated immune response to the antigenic polypeptide
CC or peptide is induced that is greater in magnitude and/or duration than
CC an immune response induced by administration of the first vector alone.
CC The invention further includes: a particle comprising a material that is
CC suitable for introduction into a cell or an animal by particle
CC bombardment, bound to which is the first and second vectors or
CC composition; a pharmaceutical composition capable of inducing or
CC enhancing an antigen specific immune response, comprising the particle
CC and a carrier or an excipient; inducing or enhancing an antigen specific
CC immune response in a subject; increasing the numbers of CD8+ CTLs
CC specific for a selected desired antigen in a subject; and inhibiting the
CC growth of a tumor in a subject. The nucleic acid composition is useful as
CC an immunogen for inhibiting the growth of a tumor, hence it has
CC cytostatic activity. This sequence represents an anti-apoptotic vector HPV

CC E6 antigenic protein of the invention.
XX SQ Sequence 158 AA;
Query Match 99.2%; Score 823; DB 9; Length 158;
Best Local Similarity 98.0%; Pred. No. 9.7e-84;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MFQDPQERPRKLPOLCTELQTTIHDIILECYCCKQQLLRREYDFAFRDLCTIVYRDGNPY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIILECYCCKQQLLRREYDFAFRDLCTIVYRDGNPY 67
QY 61 AVXDKCLKFYSKISEYRHYCYSVYGTTLQOYNKPLCDLIRCIINXQKPLCPREEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHYCYSLVGTTLQOYNKPLCDLIRCIINXQKPLCPREEKQRHLD 127
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 15
AEA98532 standard; protein; 158 AA.
XX AEA98532;
XX AEA98532;
XX 08-SEP-2005 (first entry)
DE HPV (oncogenic strain) E6 amino acid sequence SEQ ID 13.
XX Papillomavirus infection; virulence; E6 protein; diagnosis; antibody;
KM cancer; cervix tumor; cytostatic.
XX Human papillomavirus type 16.
XX US2005142541-A1.
XX 30-JUN-2005.
XX 23-DEC-2004; 2004US-00021949.
XX 23-DEC-2003; 2003US-0532373P.
XX (ARBO-) ARBOR VITA CORP.
PI Lu PS, Garman JD, Belmares MP, Somoza DC, Schweizer J;
DR WPI; 2005-457781/46.
XX New antibody composition comprising a mixture of monoclonal antibodies
PT for oncogenic strains of human papilloma virus, useful for diagnosing
PT cancer.
XX
PS Disclosure; SEQ ID NO 13; 161bp; English.
XX The invention relates to an antibody composition comprising a mixture of
CC monoclonal antibodies that specifically bind to E6 proteins of human
CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one
CC of the monoclonal antibodies specifically binds to E6 proteins of at
CC least three different oncogenic HPV strains. Also included are a
CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample,
CC comprising the antibody composition above), a method of detecting an HPV
CC E6 protein in a sample, a method of detecting the presence of an
CC oncogenic HPV E6 protein in a sample and a system for detecting the
CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a
CC first and a second binding partner for an oncogenic HPV E6 polypeptide,
CC where the first binding partner is a PDZ domain protein and the second
CC binding partner is an antibody that specifically binds to the E6 proteins
CC of at least three different oncogenic HPV strains). The antibody
CC composition, kit, methods, and system are useful for diagnosing cancer,
CC particularly cervical cancer. The present sequence is an HPV E6 protein.

SQ Sequence 158 AA;

Query Match 99.2%; Score 823; DB 9; Length 158;

Best Local Similarity 98.0%; Pred. No. 9.7e-84;

Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MFODPOERPRKL	POLCTELQTTIHDI	IEECVYCKQQL	LRREYDPAFRDL	CIYYRDGNPY	60
DB	8	MFODPOERPRKL	POLCTELQTTIHDI	IEECVYCKQQL	LRREYDPAFRDL	CIYYRDGNPY	67
QY	61	AVXDCKLKFYSK	ISEYRHYCYSVY	GTTLEQQYNKPL	CDLLIRCI	INXOKPLCP	EEKORHLD 120
DB	68	AVCDCKLKFYSK	ISEYRHYCYSLV	GTTLEQQYNKPL	CDLLIRCI	INXOKPLCP	EEKORHLD 127
QY	121	KKORFHNIRGR	WTGRGMSCCR	SSRTRETOL	151		
DB	128	KKORFHNIRGR	WTGRGMSCCR	SSRTRETOL	158		

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Job time : 223.345 secs

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OM protein - protein search, using sw model

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Title: US-10-530-253-13

Perfect score: 830
Sequence: 1 MFQDPQRRPRKLPQLCTELQ.....MTGRMCGCRSRRTRETQL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Maximum DB seq length: 2000000000

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Maximum Match 100%
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Database : Issued Patents AA:*

- 1: /EMC_Celerra_SIDS3/prodata/2/iaa/5/COMB.pep:*
- 2: /EMC_Celerra_SIDS3/prodata/2/iaa/6/COMB.pep:*
- 3: /EMC_Celerra_SIDS3/prodata/2/iaa/7/COMB.pep:*
- 4: /EMC_Celerra_SIDS3/prodata/2/iaa/H/COMB.pep:*
- 5: /EMC_Celerra_SIDS3/prodata/2/iaa/PC/US/COMB.pep:*
- 6: /EMC_Celerra_SIDS3/prodata/2/iaa/RE/COMB.pep:*
- 7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826	99.5	162	1 US-08-316-239B-4	Sequence 4, Appli
2	823	99.2	158	2 US-09-980-523A-2	Sequence 2, Appli
3	823	99.2	158	3 US-09-763-616-1	Sequence 1, Appli
4	823	99.2	162	1 US-08-316-239B-3	Sequence 3, Appli
5	823	99.2	266	2 US-08-860-165-10	Sequence 10, Appli
6	823	99.2	266	2 US-09-359-382-10	Sequence 10, Appli
7	823	99.2	266	2 US-09-367-309A-1	Sequence 1, Appli
8	823	99.2	273	2 US-09-485-885-4	Sequence 4, Appli
9	823	99.2	292	2 US-09-485-885-10	Sequence 10, Appli
10	823	99.2	371	2 US-09-485-885-6	Sequence 6, Appli
11	823	99.2	390	2 US-09-485-885-14	Sequence 14, Appli
12	818	98.6	151	2 US-09-701-080C-18	Sequence 18, Appli
13	779.5	93.9	243	2 US-09-463-993-1	Sequence 1, Appli
14	519	62.5	172	2 US-08-860-165-12	Sequence 12, Appli
15	519	62.5	172	2 US-09-359-382-12	Sequence 12, Appli
16	478	57.6	172	2 US-08-860-165-14	Sequence 14, Appli
17	478	57.6	172	2 US-09-359-382-14	Sequence 14, Appli
18	477	57.5	182	1 US-08-117-083-10	Sequence 10, Appli
19	455.5	54.9	158	1 US-08-247-904B-10	Sequence 10, Appli
20	455.5	54.9	158	2 US-08-767-942A-19	Sequence 19, Appli
21	455.5	54.9	271	1 US-08-117-083-14	Sequence 14, Appli
22	455.5	54.9	278	2 US-09-485-885-21	Sequence 21, Appli
23	455.5	54.9	383	2 US-09-485-885-23	Sequence 23, Appli
24	304	36.6	368	2 US-09-000-094-20	Sequence 20, Appli
25	304	36.6	368	2 US-10-011-749-20	Sequence 20, Appli
26	304	36.6	375	2 US-09-000-094-22	Sequence 22, Appli

27	304	36.6	375	2 US-10-011-749-22	Sequence 22, Appli
28	304	36.6	465	2 US-09-000-094-24	Sequence 24, Appli
29	304	36.6	465	2 US-10-011-749-24	Sequence 24, Appli
30	304	36.6	1587	2 US-09-000-094-46	Sequence 46, Appli
31	304	36.6	1587	2 US-10-011-749-46	Sequence 46, Appli
32	163	19.6	30	1 US-08-363-586-4	Sequence 4, Appli
33	163	19.6	30	2 US-09-980-523A-4	Sequence 4, Appli
34	159	19.2	29	2 US-09-980-523A-8	Sequence 8, Appli
35	134.5	16.2	137	2 US-09-913-204-17	Sequence 17, Appli
36	130	15.7	22	2 US-09-980-523A-10	Sequence 10, Appli
37	128	15.4	23	2 US-09-601-729-276	Sequence 276, App
38	124	14.9	22	2 US-09-980-523A-6	Sequence 6, Appli
39	120	14.5	21	1 US-08-934-915-167	Sequence 167, App
40	119	14.3	137	2 US-09-913-204-3	Sequence 3, Appli
41	119	14.3	137	2 US-09-913-204-7	Sequence 7, Appli
42	119	14.3	137	2 US-09-913-204-13	Sequence 13, Appli
43	115	13.9	32	1 US-08-934-915-166	Sequence 166, App
44	115	13.9	32	1 US-08-466-285-2	Sequence 2, Appli
45	115	13.9	32	2 US-08-164-768-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; US-08-316-239B-4
Query Match 99.5%; Score 826; DB 1; Length 162;
Best Local Similarity 98.7%; Pred. No. 8.2e-86;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MFQDPOERPRKJLPOLCTEJQTTIHDIIEECVYCKOQLLRREYDPAFFDLCTIVRDGNPY	60
Db	8	MFQDPOERPRKJLPOLCTEJQTTIHDIIEECVYCKOQLLRREYDPAFFDLCTIVRDGNPY	67
Qy	61	AVADCKLKFPSKISIEYRHYCVSYGTTLEEQYNKPLCDLLRCINXQKPLCPEEKOHL	120
Db	68	AVDCKLKFPSKISIEYRHYCVSYGTTLEEQYNKPLCDLLRCINXQKPLCPEEKOHL	127
Qy	121	KKQRFNINIRGWTGRCMSCCRSRTRETFOL	151
Db	128	KKQRFNINIRGWTGRCMSCCRSRTRETFOL	158

```

RESULT 2
US-09-980-523A-2
: Sequence 2, Application US/0980523A
: Patent No. 6783763
: GENERAL INFORMATION:
: APPLICANT: CHOUPIN, JEANNINE
: APPLICANT: BOURGAULT VILLADA, ISABELLE
: APPLICANT: GUILLET, JEAN-GERARD
: APPLICANT: CONNAN, FRANCINE
: APPLICANT: FERRIES, ESTELLE
: TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
: TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
: TITLE OF INVENTION: PARTICULARLY IN VACCINATION
: FILE REFERENCE: WO/01/40105
: CURRENT APPLICATION NUMBER: US/09/980,523A
: CURRENT FILING DATE: 2002-04-29
: PRIOR APPLICATION NUMBER: PCT/FR00/01513
: PRIOR FILING DATE: 2000-05-31
: PRIOR APPLICATION NUMBER: FR 99/07012
: PRIOR FILING DATE: 1999-06-03
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2
: LENGTH: 158
: TYPE: PRT
: ORGANISM: Human Papillomavirus
: RS-09-980-523A-2

```

```

Query Match      99.2%; Score 823; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.7e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0

QY      1 MFQDPOERPKL.PQLTLEQTTTHDILIECVYCKOOLLRREYVDPAPFGLCTIVRDNPY 60
Db      8 MFQDPOERPKL.PQLTLEQTTTHDILIECVYCKOOLLRREYVDPAPFGLCTIVRDNPY 67

QY      61 AVADCKLKFYSKISEYRHYCVSYVGTTLLEQOYNKPLCDLLIRCIINXOKPLCPBEKQHL 120
Db      68 AVCDCKLKFYSKISEYRHYCVSYVGTTLLEQOYNKPLCDLLIRCIINQKPLCPBEKQHL 127

QY      121 KKQPFNIRGRTWGRCMSCCRSRPRRETOL 151
Db      128 KKQPFNIRGRTWGRCMSCCRSRIRRETOL 158

RESULT 3
US-09-763-616-1
; Sequence 1, Application US/09763616
; Patent No. 7019000
; GENERAL INFORMATION:
; APPLICANT: BERNARD, HANS-ULRICH
; APPLICANT: TAN, YEE JOO
; APPLICANT: BEERHEIDE, WALTER
; APPLICANT: SIM, ANTHONY EUGENE
; APPLICANT: SIM, MUI MUI
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS AND METHODS
; FILE REFERENCE: BERN3001/JDB
; CURRENT APPLICATION NUMBER: US/09/763, 616
; CURRENT FILING DATE: 2001-05-16
; PRIORITY APPLICATION NUMBER: PCT/AU99/00724

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? PRIOR FILING DATE: 1999-09-03
? PRIOR APPLICATION NUMBER: AU P01645/99
? PRIOR FILING DATE: 1999-07-15
? PRIOR APPLICATION NUMBER: AU P5733/98
? PRIOR FILING DATE: 1998-09-04
? NUMBER OF SEQ ID NOS: 2
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO: 1
? LENGTH: 158
? TYPE: PRF
? ORGANISM: Human papillomavirus type 16
US-09-763-616-1

```

	Query Match	Best Local Similarity	Score 823;	DB 3;	Length 158;
	Matches 148;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	MFODPOERPRKL	POLCETELQTTIHDIIL	ECVYCKQOOLLIRREYVDP	PAFRDLCTIVRDGPNY 60
Dy	8	MFODPOERPRKL	POLCETELQTTIHDIIL	ECVYCKQOOLLIRREYVDP	PAFRDLCTIVRDGPNY 67
Qy	61	AVNDKCLKLFPSKIS	SEYHHYCGSVYGTLL	LEQYNNKPLCDLLIRCN	NXQKPLCPBEKQRHLD 120
Dy	68	AVCDKCLKLFPSKIS	SEYHHYCGSVYGTLL	LEQYNNKPLCDLLIRCN	COKPLCPBEKQRHLD 127
Qy	121	KKQRFHHIRGRMTGR	CMSCCRSSRTRETOI		151
Dy	128	KKQRFHHIRGRMTGR	CMSCCRSSRTRETOI		158

RESULT 4
 US-08-316-2398-3
 : Sequence 3, Application US/08316239B
 : Patent No. 5678509
 : GENERAL INFORMATION:
 APPLICANT: Wheeler, Cosette M.
 APPLICANT: Parmenter, Cheryl A.
 TITLE OF INVENTION: Methods and a Diagnostic Aid for
 TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
 TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
 TITLE OF INVENTION: Cervical Cancer
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jagtiani & Associates
 STREET: 6126 Rocky Way Court
 CITY: Centreville
 STATE: VA
 COUNTRY: USA
 ZIP: 20120-3400
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/316,239B
 FILING DATE: 30-SEP-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jagtiani, Ajay A.
 REGISTRATION NUMBER: 35,205
 REFERENCE/DOCKET NUMBER: UNME-0001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 817-9453
 TELEFAX: (703) 803-9387
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 162 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO

US-08-316-239B-3

Query Match 99.2%; Score 823; DB 1; Length 162;
Best Local Similarity 98.0%; Pred. No. 1.8e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 67
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGWRGCMSCCRSSRTRETOL 158

RESULT 5

US-08-860-165-10
Sequence 10, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:

APPLICANT: EDWARDS, Scitling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT FILING DATE: 1997-09-22
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 99.2%; Score 823; DB 2; Length 266;
Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 67
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGWRGCMSCCRSSRTRETOL 158

RESULT 6

US-09-359-382-10

Sequence 10, Application US/09359382
Patent No. 6306397
GENERAL INFORMATION:
APPLICANT: EDWARDS, Scitling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PNO157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 99.2%; Score 823; DB 2; Length 266;
Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 67
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGWRGCMSCCRSSRTRETOL 158

RESULT 7

US-09-367-309A-1

Sequence 1, Application US/09367309A
Patent No. 6428807
GENERAL INFORMATION:
APPLICANT: MACFARLAN, RODERICK I.
APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 2; Length 266;
Best Local Similarity 98.0%; Pred. No. 3.2e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYVDFAFDLCIVRDGNPY 67
QY 61 AVXDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGWRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGWRGCMSCCRSSRTRETOL 158

```
RESULT 8
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4
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Query Match          99.2%; Score 823; DB 2; Length 273;
Best Local Similarity 98.0%; Pred. No. 3.3e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFRDLCIVYRDGPNPY 60
Db      114 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFRDLCIVYRDGPNPY 173

Qy      61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
Db      174 AVCDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 233

Qy      121 KKORFHNIRGRWTRCSCCRSSRTTRRETOL 151
Db      234 KKORFHNIRGRWTRCSCCRSSRTTRRETOL 264
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RESULT 9
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
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Query Match          99.2%; Score 823; DB 2; Length 292;
Best Local Similarity 98.0%; Pred. No. 3.6e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFRDLCIVYRDGPNPY 60
Db      133 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFRDLCIVYRDGPNPY 192

Qy      61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
Db      193 AVCDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 252

Qy      121 KKORFHNIRGRWTRCSCCRSSRTTRRETOL 151
Db      253 KKORFHNIRGRWTRCSCCRSSRTTRRETOL 283
```

```
RESULT 10
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6
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```
Query Match          99.2%; Score 823; DB 2; Length 371;
Best Local Similarity 98.0%; Pred. No. 4.8e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFRDLCIVYRDGPNPY 60
Db      114 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFAFRDLCIVYRDGPNPY 173

Qy      61 AVXDCKLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 120
Db      174 AVCDKCLKFYSKISEYRHVCYSVYGTLEQYNNKPLCDLLIRICINXOKPLCPBEKQRLD 233

Qy      121 KKORFHNIRGRWTRCSCCRSSRTTRRETOL 151
Db      234 KKORFHNIRGRWTRCSCCRSSRTTRRETOL 264
```

```
RESULT 11
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
```

;; PRIOR APPLICATION NUMBER: GB 9717953.5
;; PRIOR FILING DATE: 1997-08-22
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 14
;; LENGTH: 390
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 99.2%; Score 823; DB 2; Length 390;
Best Local Similarity 98.0%; Pred. No. 5,1e-85;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60
DB 133 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 192
QY 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPEEKQRHLD 120
DB 193 AVXDCKLFYSKISSEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPEEKQRHLD 252
QY 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151
DB 253 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 283

RESULT 12
US-09-701-080C-18
;; Sequence 18, Application US/09701080C
;; Patent No. 6864054

;; GENERAL INFORMATION:
;; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
;; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P300 F
;; FILE REFERENCE: N73477C GCM
;; CURRENT APPLICATION NUMBER: US/09/701,080C
;; PRIOR FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: GB 9811303.8
;; PRIOR FILING DATE: 1998-05-26
;; PRIOR APPLICATION NUMBER: GB 9900157.0
;; PRIOR FILING DATE: 1999-01-05
;; NUMBER OF SEQ ID NOS: 36
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 18
;; LENGTH: 151
;; TYPE: PRT
;; ORGANISM: Human papillomavirus
US-09-701-080C-18

Query Match 98.6%; Score 818; DB 2; Length 151;
Best Local Similarity 97.4%; Pred. No. 6,1e-85;
Matches 147; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60
DB 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60
QY 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPEEKQRHLD 120
DB 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPEEKQRHLD 120
QY 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151
DB 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151

RESULT 13
US-09-462-993-1
;; Sequence 1, Application US/09462993
;; Patent No. 6884786
;; GENERAL INFORMATION:
;; APPLICANT: KIEVY, Marie-Paule

;; APPLICANT: BAILLOU, Jean-Marc
;; APPLICANT: BIZOUARNE, Nadine
;; TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
;; TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
;; FILE REFERENCE: 01753-122
;; CURRENT APPLICATION NUMBER: US/09/462,993
;; PRIOR FILING DATE: 2000-04-17
;; PRIOR APPLICATION NUMBER: PCT/FR98/01576
;; PRIOR FILING DATE: 1998-07-17
;; PRIOR APPLICATION NUMBER: FR 97/09152
;; PRIOR FILING DATE: 1997-07-18
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: PatentIn Ver. 2.2
;; SEQ ID NO 1
;; LENGTH: 243
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Derived from
;; OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein
;; OTHER INFORMATION: fused F protein signals, clone B6*TWf.
US-09-462-993-1

Query Match 93.9%; Score 779.5; DB 2; Length 243;
Best Local Similarity 94.7%; Pred. No. 2,5e-80;
Matches 143; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 60
DB 36 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLDLCIVRDGPNY 95
QY 61 AVXDCKLFYSKISSEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPEEKQRHLD 120
DB 96 AVXDCKLFYSKISSEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPEEKQRHLD 150
QY 121 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 151
DB 151 KKORFHNIRGRWTCGMSCCRSSRTRRETOL 181

RESULT 14
US-08-860-165-12
;; Sequence 12, Application US/08860165A
;; Patent No. 6004557

;; GENERAL INFORMATION:
;; APPLICANT: EDWARDS, Scirling John
;; APPLICANT: COX, John Cooper
;; APPLICANT: WEBB, Elizabeth Ann
;; APPLICANT: FRATER, Ian
;; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
;; FILE REFERENCE: 17227/130
;; CURRENT APPLICATION NUMBER: US/08/860,165A
;; PRIOR FILING DATE: 1997-09-22
;; EARLIER APPLICATION NUMBER: PCT/AU95/00868
;; EARLIER FILING DATE: 1995-12-20
;; EARLIER FILING DATE: 1994-12-20.
;; NUMBER OF SEQ ID NOS: 15
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 12
;; LENGTH: 172
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 62.5%; Score 519; DB 2; Length 172;
Best Local Similarity 96.8%; Pred. No. 5,7e-51;
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPFAVXDCKLFYSKISSEYRHVCYSVGTTLBOQYNKPLCDLLIRICINXQKPLCPEEKQRHLD 116

Db 2 GNPYAVCDKCLKFYSKISEYRHYCYSLYGTTLLEOQYNNKPLCDLLIRCIINCQKPLCPBEKQ 61

QY 117 RHLDKQRFHNIRGRMTGRCMSCCRSSSTRRETQL 151

Db 62 RHLDKQRFHNIRGRMTGRCMSCCRSSSTRRETQL 96

RESULT 15

US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 62.5%; Score 519; DB 2; Length 172;
Best Local Similarity 96.8%; Pred. No. 5.7e-51;
Matches 92; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 57 GNPYAVCDKCLKFYSKISEYRHYCYSLYGTTLLEOQYNNKPLCDLLIRCIINCQKPLCPBEKQ 116

Db 2 GNPYAVCDKCLKFYSKISEYRHYCYSLYGTTLLEOQYNNKPLCDLLIRCIINCQKPLCPBEKQ 61

QY 117 RHLDKQRFHNIRGRMTGRCMSCCRSSSTRRETQL 151

Db 62 RHLDKQRFHNIRGRMTGRCMSCCRSSSTRRETQL 96

Search completed: June 6, 2006, 12:13:14
Job time : 45.2691 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:10 ; Search time 164.341 Seconds
(without alignments)
425.611 Million cell updates/sec

Title: US-10-530-253-13

Perfect score: 830

Sequence: 1 MFQDPQERPRKLPOLCTELQ.....WTGRCMSCCSSRRTRRETOL 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications MA Main:*

- 1: /EMC_CeJerra_SIDS3/ptocdata/2/pubppa/US07_PUBCOMB.pep:*
- 2: /EMC_CeJerra_SIDS3/ptocdata/2/pubppa/US08_PUBCOMB.pep:*
- 3: /EMC_CeJerra_SIDS3/ptocdata/2/pubppa/US09_PUBCOMB.pep:*
- 4: /EMC_CeJerra_SIDS3/ptocdata/2/pubppa/US10_PUBCOMB.pep:*
- 5: /EMC_CeJerra_SIDS3/ptocdata/2/pubppa/US10_PUBCOMB.pep:*
- 6: /EMC_CeJerra_SIDS3/ptocdata/2/pubppa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	828	99.8	248 5	US-10-530-253-3
2	828	99.8	248 5	US-10-530-253-5
3	826	99.5	151 5	US-10-484-063-20
4	826	99.5	151 5	US-10-484-063-27
5	826	99.5	151 5	US-10-530-253-13
6	826	99.5	248 5	US-10-530-253-1
7	823	99.2	158 5	US-10-858-384-2
8	823	99.2	158 5	US-10-367-057-16
9	823	99.2	158 6	US-11-021-949-13
10	823	99.2	158 6	US-11-021-949-13
11	823	99.2	171 4	US-10-472-724-2
12	823	99.2	248 5	US-10-530-253-9
13	823	99.2	248 5	US-10-530-253-11
14	823	99.2	256 6	US-11-192-923A-2
15	823	99.2	266 3	US-09-367-309A-1
16	823	99.2	273 4	US-10-000-903-4
17	823	99.2	273 4	US-10-899-771-4
18	823	99.2	292 4	US-10-000-903-10
19	823	99.2	292 4	US-10-899-771-10
20	823	99.2	371 5	US-10-000-903-6
21	823	99.2	371 5	US-10-899-771-6
22	823	99.2	390 4	US-10-000-903-14
23	823	99.2	390 4	US-10-899-771-14
24	821	98.9	248 5	US-10-530-253-7
25	819	98.7	151 4	US-10-177-390-6
26	779.5	93.9	243 6	US-11-072-288-1
27	578	69.6	149 5	US-10-530-253-18

28	578	69.6	149 6	US-11-021-949-14	Sequence 14, Appl
29	523	63.0	149 5	US-10-530-253-16	Sequence 16, Appl
30	523	63.0	149 6	US-11-021-949-18	Sequence 18, Appl
31	520	62.7	149 5	US-10-530-253-17	Sequence 17, Appl
32	520	62.7	149 6	US-11-021-949-16	Sequence 16, Appl
33	498	60.0	149 6	US-11-021-949-160	Sequence 360, App
34	496	59.8	149 5	US-10-530-253-24	Sequence 24, Appl
35	496	59.8	149 6	US-11-021-949-15	Sequence 15, Appl
36	487	58.7	148 6	US-10-530-253-12	Sequence 22, Appl
37	487	58.7	148 6	US-11-021-949-17	Sequence 17, Appl
38	484	58.3	148 6	US-11-021-949-359	Sequence 359, App
39	483	58.2	148 6	US-11-021-949-19	Sequence 19, Appl
40	468.5	56.4	158 6	US-10-530-253-26	Sequence 26, Appl
41	468.5	56.4	158 6	US-11-021-949-361	Sequence 361, App
42	460	55.4	151 5	US-10-530-253-21	Sequence 21, Appl
43	460	55.4	151 6	US-11-021-949-24	Sequence 24, Appl
44	459.5	55.4	158 5	US-10-530-253-20	Sequence 20, Appl
45	459.5	55.4	158 6	US-11-021-949-29	Sequence 29, Appl

ALIGNMENTS

```
RESULT 1
US-10-530-253-3
; Sequence 3, Application US/10530253
; Publication No. US20060014926a1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; PRIOR FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-3

Query Match      99.8%; Score 828; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 6.5e-81;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MFQDPQERPRKLPOLCTELQTTIHDIILIECYCKQQLLRREYDFAFRDLCTIVRDGMPY 60
DB      1 MFQDPQERPRKLPOLCTELQTTIHDIILIECYCKQQLLRREYDFAFRDLCTIVRDGMPY 60
QY      61 AVDXKCIKFYSKISEYRRYCYVYGTTLBQYKPLCDLLIRCIKXQKPLCPBEKORHLD 120
DB      61 AVDXKCIKFYSKISEYRRYCYVYGTTLBQYKPLCDLLIRCIKXQKPLCPBEKORHLD 120
QY      121 KQRFHNIRGWRGRCMSCCSSRRTRRETOL 151
DB      121 KQRFHNIRGWRGRCMSCCSSRRTRRETOL 151

RESULT 2
US-10-530-253-5
; Sequence 5, Application US/10530253
; Publication No. US20060014926a1
; GENERAL INFORMATION:
; APPLICANT: Casasetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
```


QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 60
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
DB 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 6
US-10-530-253-1

; Sequence 1, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-1

Query Match 99.5%; Score 826; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 1.1e-80;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 60
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
DB 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151

RESULT 7
US-10-858-384-2

; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012

; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 99.2%; Score 823; DB 5; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 67
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
DB 68 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 8
US-10-367-057-16

; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuttilli, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Cnaseqdist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 99.2%; Score 823; DB 5; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYVDFAFRDLCTIVRDGPNY 67
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 120
DB 68 AVXDCKLKFYSKISEYRHYCYSVYGTLEQOYNKPLCDLLIRCTINXOKPLCPBEKQRHLD 127
QY 121 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 151
DB 128 KKQRFHNIRGRWTRGCMSCCRSSRTRETOL 158

RESULT 9
US-11-021-949-13

; Sequence 13, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
; APPLICANT: LU, PETER
; APPLICANT: GARMAN, JONATHAN DAVID

```
; APPLICANT: BELMARES, MICHAEL P
; APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
; APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; FILE REFERENCE: VITA-012
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-13
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Query Match          99.2%; Score 823; DB 6; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Db 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLIRICINXOKPLCPBEKQRLHD 120
Db 68 AVCDCKLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLIRICINXOKPLCPBEKQRLHD 127
Qy 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151
Db 128 KKORFHNIRGRWTCRSCCSSRTRRETOL 158
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RESULT 10
US-11-206-138-3
; Sequence 3, Application US/11206138
; Publication No. US2006003919A1
; GENERAL INFORMATION:
; APPLICANT: Healthbanc Biotech CO. LTD.
; TITLE OF INVENTION: Fusion protein for inhibiting cervical cancer
; FILE REFERENCE: P7819/0613
; CURRENT APPLICATION NUMBER: US/11/206,138
; CURRENT FILING DATE: 2005-08-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 3
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-11-206-138-3
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Query Match          99.2%; Score 823; DB 6; Length 158;
Best Local Similarity 98.0%; Pred. No. 1.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Db 8 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLIRICINXOKPLCPBEKQRLHD 120
Db 68 AVCDCKLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLIRICINXOKPLCPBEKQRLHD 127
Qy 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151
Db 128 KKORFHNIRGRWTCRSCCSSRTRRETOL 158
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RESULT 11
US-10-472-724-2
; Sequence 2, Application US/10472724
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; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HIV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
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Query Match          99.2%; Score 823; DB 4; Length 171;
Best Local Similarity 98.0%; Pred. No. 1.5e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 60
Db 13 MFODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 72
Qy 61 AVXDCKLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLIRICINXOKPLCPBEKQRLHD 120
Db 73 AVCDCKLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLIRICINXOKPLCPBEKQRLHD 132
Qy 121 KKORFHNIRGRWTCRSCCSSRTRRETOL 151
Db 133 KKORFHNIRGRWTCRSCCSSRTRRETOL 163
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RESULT 12
US-10-530-253-9
; Sequence 9, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Casaretti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-9
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Query Match          99.2%; Score 823; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 2.2e-80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 FODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 61
Db 99 FODPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCTIVRDGPNY 158
Qy 62 VXDCKLKFYSKISEYRHVCYSVGTTLLEQOYNKPLCDLIRICINXOKPLCPBEKQRLHD 121
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Db 159 VGDCKLKFYSKISEYRHVCYSLVGTTLLEQYNKPLCDLLIRCIHQKPLCPBEKORHLDK 218
Qy 122 KORFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 219 KORFHNIRGWTGRCMSCCRSSRTRETOL 248

RESULT 13
US-10-530-253-11
; Sequence 11, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassecci, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan P. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530,253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-11

Query Match 99.2%; Score 823; DB 5; Length 248;
Best Local Similarity 98.7%; Pred. No. 2.2e-80;
Matches 148; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTIVRDGNPY 61
Db 99 FODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTIVRDGNPY 158
Qy 62 VXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNKPLCDLLIRCIHQKPLCPBEKORHLDK 121
Db 159 VGDCKLKFYSKISEYRHVCYSLVGTTLLEQYNKPLCDLLIRCIHQKPLCPBEKORHLDK 218
Qy 122 KORFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 219 KORFHNIRGWTGRCMSCCRSSRTRETOL 248

RESULT 14
US-11-192-923A-2
; Sequence 2, Application US/11192923A
; Publication No. US20060018928A1
; GENERAL INFORMATION:
; APPLICANT: PAN, XIAOWU
; TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS
; FILE REFERENCE: 116620-003
; CURRENT APPLICATION NUMBER: US/11/192,923A
; CURRENT FILING DATE: 2005-07-29
; PRIOR APPLICATION NUMBER: CN 03115272.4
; PRIOR FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: CN 03115273.2
; PRIOR FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 2
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-11-192-923A-2

Query Match 99.2%; Score 823; DB 6; Length 256;
Best Local Similarity 98.0%; Pred. No. 2.3e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTIVRDGNPY 60
Db 106 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTIVRDGNPY 165
Qy 61 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNKPLCDLLIRCIHQKPLCPBEKORHLD 120
Db 166 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNKPLCDLLIRCIHQKPLCPBEKORHLD 225
Qy 121 KORFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 226 KORFHNIRGWTGRCMSCCRSSRTRETOL 256

RESULT 15
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 99.2%; Score 823; DB 3; Length 266;
Best Local Similarity 98.0%; Pred. No. 2.4e-80;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTIVRDGNPY 60
Db 8 MFODPOERPRKLPOLCTELQTTIHDIIECVYCKQQLLRREYDPAFRDLCTIVRDGNPY 67
Qy 61 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNKPLCDLLIRCIHQKPLCPBEKORHLD 120
Db 68 AVXDCKLKFYSKISEYRHVCYSLVGTTLLEQYNKPLCDLLIRCIHQKPLCPBEKORHLD 127
Qy 121 KORFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 128 KORFHNIRGWTGRCMSCCRSSRTRETOL 158

Search completed: June 6, 2006, 12:32:59
Job time : 164.341 secs

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OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:35 ; Search time 10.9157 Seconds
(without alignments)
159.985 Million cell updates/sec

Title: US-10-530-253-13

Perfect score: 830
Sequence: 1 MFQDPQRPRKRLPOLCTELQ.....MTGRCMSCRSRRRTRELQ 151

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*

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- 8: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US00_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	114	13.7	22 7 US-11-209-206-4	Sequence 4, Appli
2	74.5	9.0	590 7 US-11-223-610-1	Sequence 1, Appli
3	74.5	9.0	591 6 US-10-933-854-4	Sequence 4, Appli
4	74.5	9.0	591 6 US-10-933-854-6	Sequence 6, Appli
5	74.5	9.0	600 6 US-10-933-854-2	Sequence 2, Appli
6	72.5	8.7	800 6 US-10-953-349-33871	Sequence 33871, A
7	72.5	8.7	809 6 US-10-953-349-33870	Sequence 33870, A
8	72.5	8.7	867 6 US-10-953-349-33869	Sequence 33869, A
9	71	8.6	531 6 US-11-293-697-2762	Sequence 2762, Ap
10	68	8.2	22 7 US-11-209-206-5	Sequence 5, Appli
11	65	7.8	369 6 US-10-953-349-17182	Sequence 17182, A
12	63.5	7.7	419 6 US-10-953-349-6306	Sequence 6306, Ap
13	63.5	7.7	515 6 US-10-953-349-6305	Sequence 6305, Ap
14	63.5	7.7	540 6 US-10-953-349-6304	Sequence 6304, Ap
15	63	7.6	247 6 US-10-953-349-32521	Sequence 32521, A
16	63	7.6	276 6 US-10-953-349-32520	Sequence 32520, A
17	63	7.6	307 6 US-10-953-349-32519	Sequence 32519, A
18	62.5	7.5	278 7 US-11-293-697-4876	Sequence 4876, Ap
19	62.5	7.5	472 7 US-11-106-014-8	Sequence 8, Appli
20	62	7.5	417 6 US-10-196-749-474	Sequence 474, App
21	62	7.5	1056 6 US-10-505-928-225	Sequence 225, App
22	61.5	7.4	176 6 US-10-953-349-18091	Sequence 18091, A
23	61.5	7.4	208 6 US-10-953-349-18090	Sequence 18090, A
24	61.5	7.4	220 6 US-10-953-349-18089	Sequence 18089, A
25	61.5	7.4	705 7 US-11-293-697-4346	Sequence 4346, Ap

26	61	7.3	259 6 US-10-953-349-19918	Sequence 19918, A
27	61	7.3	355 6 US-10-953-349-19917	Sequence 19917, A
28	60.5	7.3	267 6 US-10-953-349-28497	Sequence 28497, A
29	60.5	7.3	314 6 US-10-538-066-365	Sequence 365, App
30	60.5	7.3	706 7 US-11-293-697-3919	Sequence 3919, App
31	60.5	7.3	971 6 US-10-505-928-397	Sequence 397, App
32	60.5	7.3	1085 6 US-10-505-928-175	Sequence 175, App
33	60	7.2	867 6 US-11-293-697-1034	Sequence 3034, Ap
34	59	7.1	233 6 US-10-953-349-13389	Sequence 13389, A
35	59	7.1	258 6 US-10-953-349-1032	Sequence 1032, Ap
36	59	7.1	369 6 US-10-953-349-1031	Sequence 1031, Ap
37	59	7.1	376 6 US-10-953-349-1030	Sequence 1030, Ap
38	59	7.1	385 6 US-10-953-349-13388	Sequence 13388, A
39	59	7.1	400 6 US-10-953-349-13387	Sequence 13387, A
40	59	7.1	428 6 US-10-953-349-25008	Sequence 25008, A
41	59	7.1	433 6 US-10-953-349-25007	Sequence 25007, A
42	59	7.1	436 6 US-10-953-349-25006	Sequence 25006, A
43	58.5	7.0	204 6 US-10-953-349-37463	Sequence 37463, A
44	58.5	7.0	251 6 US-10-953-349-38140	Sequence 38140, A
45	58.5	7.0	280 6 US-10-953-349-38139	Sequence 38139, A

ALIGNMENTS

RESULT 1
US-11-209-206-4
Sequence 4, Application US/11209206
Publication No. US20060110794A1
GENERAL INFORMATION:
APPLICANT: Impact Diagnostics
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi
TITLE OF INVENTION: Associated Cancers
FILE REFERENCE: 3352-2-2
CURRENT APPLICATION NUMBER: US/11/209, 206
CURRENT FILING DATE: 2005-08-22
PRIOR APPLICATION NUMBER: US 60/394, 172
PRIOR FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: US 09/828, 645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
US-11-209-206-4
Query Match 13.7%; Score 114; DB 7; Length 22;
Best Local Similarity 95.5%; Pred. No. 3.7e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 55 RDGNPVAVXDCKLKFYSKISEY 76
Db 1 RDGNPVAVCDCKLKFYSKISEY 22
RESULT 2
US-11-223-610-1
Sequence 1, Application US/11223610
Publication No. US20060111289A1
GENERAL INFORMATION:
APPLICANT: Miziejewski, Gerald J.
TITLE OF INVENTION: Compositions and Methods of Using Alpha-Fetoprotein Growth
TITLE OF INVENTION: Inhibitory Peptides
FILE REFERENCE: HOLLAND-09516
CURRENT APPLICATION NUMBER: US/11/223, 610
CURRENT FILING DATE: 2005-09-09
NUMBER OF SEQ ID NOS: 181

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SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 590
TYPE: PRT
ORGANISM: Homo sapiens
US-11-223-610-1
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Query Match
Best Local Similarity 9.0%; Score 74.5; DB 7; Length 590;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;
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QY 6 QERPRKLPOLCTEYQTTHIDIIIECVYCKQQLLRREYVDFAFRDLCTIVY-----54
DB 260 QDGEKIMSYICSQ-QDTLSNKITEC--CKLTTL-----RQCIIHANDEKPEGLS 308
QY 55 -----RDGNPYAVXDKCLKFYKISEY--RHYCYSVYGTLEQOYNKPLCDLLIRC 103
DB 309 PNLNRFGLDRDFNPFSSGSEKNIFLASFVHEYSRHRPQLAV---SVILRVAKGYQELLEKC 365
QY 104 INXOKPL-C---PEEKORHLDDKKQ 123
DB 366 FQTEPNPLECODKGEHELOKXYIQESQ 390
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RESULT 3
US-10-933-854-4
Sequence 4, Application US/10933854
Publication No. US20060105347A1
GENERAL INFORMATION:
APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: Meade, Harry
APPLICANT: Cox, Geoffrey F.
TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammal
```

```
FILE REFERENCE: GTC-220 PCT
CURRENT APPLICATION NUMBER: US/10/933,854
PRIOR FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/500,910
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 591
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Human Alpha Fetoprotein
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/Acession No. V01514
DATABASE ENTRY DATE: 1995-03-30
RELEVANT RESIDUES: (19)..(609)
US-10-933-854-4
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Query Match
Best Local Similarity 9.0%; Score 74.5; DB 6; Length 591;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;
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QY 6 QERPRKLPOLCTEYQTTHIDIIIECVYCKQQLLRREYVDFAFRDLCTIVY-----54
DB 261 QDGEKIMSYICSQ-QDTLSNKITEC--CKLTTL-----RQCIIHANDEKPEGLS 309
QY 55 -----RDGNPYAVXDKCLKFYKISEY--RHYCYSVYGTLEQOYNKPLCDLLIRC 103
DB 310 PNLNRFGLDRDFNPFSSGSEKNIFLASFVHEYSRHRPQLAV---SVILRVAKGYQELLEKC 366
QY 104 INXOKPL-C---PEEKORHLDDKKQ 123
DB 367 FQTEPNPLECODKGEHELOKXYIQESQ 391
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RESULT 4
US-10-933-854-6
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Sequence 6, Application US/10933854
Publication No. US20060105347A1
GENERAL INFORMATION:
APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: Meade, Harry
APPLICANT: Cox, Geoffrey F.
TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammal
FILE REFERENCE: GTC-220 PCT
CURRENT APPLICATION NUMBER: US/10/933,854
PRIOR FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/500,910
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6
LENGTH: 591
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Human Alpha Fetoprotein
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/Acession No. V01514
DATABASE ENTRY DATE: 1995-03-30
RELEVANT RESIDUES: (19)..(609)
US-10-933-854-6
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Query Match
Best Local Similarity 9.0%; Score 74.5; DB 6; Length 591;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;
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QY 6 QERPRKLPOLCTEYQTTHIDIIIECVYCKQQLLRREYVDFAFRDLCTIVY-----54
DB 261 QDGEKIMSYICSQ-QDTLSNKITEC--CKLTTL-----RQCIIHANDEKPEGLS 309
QY 55 -----RDGNPYAVXDKCLKFYKISEY--RHYCYSVYGTLEQOYNKPLCDLLIRC 103
DB 310 PNLNRFGLDRDFNPFSSGSEKNIFLASFVHEYSRHRPQLAV---SVILRVAKGYQELLEKC 366
QY 104 INXOKPL-C---PEEKORHLDDKKQ 123
DB 367 FQTEPNPLECODKGEHELOKXYIQESQ 391
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RESULT 5
US-10-933-854-2
```

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Sequence 2, Application US/10933854
Publication No. US20060105347A1
GENERAL INFORMATION:
APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: Meade, Harry
APPLICANT: Cox, Geoffrey F.
TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammal
FILE REFERENCE: GTC-220 PCT
CURRENT APPLICATION NUMBER: US/10/933,854
PRIOR FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/500,910
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 609
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Human Alpha Fetoprotein
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/Acession No. V01514
DATABASE ENTRY DATE: 1995-03-30
RELEVANT RESIDUES: (1)..(609)
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US-10-933-854-2

Query Match 9.0%; Score 74.5; DB 6; Length 609;
Best Local Similarity 23.4%; Pred. No. 1.7;
Matches 34; Conservative 26; Mismatches 44; Indels 41; Gaps 8;

QY 6 QERPRKLPOLCTELQTTIHDIILCEVCYCKQQLRREVDFAFRDLCTIV----- 54
DB 279 QDEKINSYICSO-ODTISNKTIBC-CKLTLE-----RGOCITHAENDEKPEGIS 327
QY 55 -----RDGNPYAVXDKCLKFYSKISEY--RHVCYSVGTTLQOQYNNKPLCDLLIRC 103
DB 328 PNLNRFLDDRDFQNGSSGEKQNIPLASFVHEYSRRHRLQALV---SVTLVAKGYQDLLEKC 384
QY 104 INXQKPL-C---PBEKQPHLDKQ 123
DB 385 FQTEPNPECCODKGEELQKYIOESQ 409

RESULT 6

US-10-953-349-33871
; Sequence 33871, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 33871
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33871

Query Match 8.7%; Score 72.5; DB 6; Length 800;
Best Local Similarity 23.3%; Pred. No. 3.8;
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DQSRPRKLPOLCTELQTTIHDIILCEVCYCKQ-----LRRREV---DFAFRDLCTIV 54
DB 460 DDNADPSPKSKCSNRSRTVVERNLQTPPKQSHMSTSLAKCHPLOSTFASPVC--- 516
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLQOQ- 91
DB 517 ---NPVGENEKCADVTHIIFPSKILKLAIRIRNLCEVQCVGEQTERVYNNFKQILBQOT 573
QY 92 ---YNNKPLCDLLIRCINXQKPLCPBE 114
DB 574 TLFENRHIDQLILCLCYGVAKVCQLE 599

RESULT 7

US-10-953-349-33870
; Sequence 33870, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 33870
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33870

Query Match 8.7%; Score 72.5; DB 6; Length 809;
Best Local Similarity 23.3%; Pred. No. 3.8;
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DQSRPRKLPOLCTELQTTIHDIILCEVCYCKQ-----LRRREV---DFAFRDLCTIV 54
DB 469 DDNADPSPKSKCSNRSRTVVERNLQTPPKQSHMSTSLAKCHPLOSTFASPVC--- 525
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLQOQ- 91
DB 526 ---NPVGENEKCADVTHIIFPSKILKLAIRIRNLCEVQCVGEQTERVYNNFKQILBQOT 582
QY 92 ---YNNKPLCDLLIRCINXQKPLCPBE 114
DB 583 TLFENRHIDQLILCLCYGVAKVCQLE 608

RESULT 8

US-10-953-349-33869
; Sequence 33869, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953.349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 33869
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-33869

Query Match 8.7%; Score 72.5; DB 6; Length 867;
Best Local Similarity 23.3%; Pred. No. 4.1;
Matches 34; Conservative 22; Mismatches 49; Indels 41; Gaps 7;

QY 4 DQSRPRKLPOLCTELQTTIHDIILCEVCYCKQ-----LRRREV---DFAFRDLCTIV 54
DB 527 DDNADPSPKSKCSNRSRTVVERNLQTPPKQSHMSTSLAKCHPLOSTFASPVC--- 583
QY 55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLQOQ- 91
DB 584 ---NPVGENEKCADVTHIIFPSKILKLAIRIRNLCEVQCVGEQTERVYNNFKQILBQOT 640
QY 92 ---YNNKPLCDLLIRCINXQKPLCPBE 114
DB 641 TLFENRHIDQLILCLCYGVAKVCQLE 666

RESULT 9

US-11-293-697-2762
; Sequence 2762, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NOVEL FULL LENGTH CDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293.697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2762
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2762

Query March	8.6%;	Score 71;	DB 7;	Length 531;
Best Local Similarity	22.0%;	Pred. No. 3.5;	55;	Indels 28;
Matches	28;	Conservative 16;	Mismatches 16;	Gaps 5;
QY	28	LECVYCKO--OLLRREVVYDFAFRLDCLIVRDGNPYAVXDKCLKPYSKISSEYRHYCYSVYG	85	
Db	175	LGCKRCKSCGLTINAE-----YISKDGLPYCEADYHAKGIRCDSCBK---ITG	221	
QY	86	TTLE--QQYNNPLCDLIRCIHXOKPLCPBEKORHLDKQRFNNIRGWTGRCHSCCSS	143	
Db	222	RVLAGEGKHYPSCALCVGC-----GQMFAGEEEMYLQSSSIWHPACROAPTE	270	
QY	144	RTRETO	150	
Db	271	DRNKETR	277	

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RESULT 10
US-11-209-206-5
; Sequence 5, Application US/11209206
; Publication No. US20060110794A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Pap
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/11/209,206
; CURRENT FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 18
US-11-209-206-5

Query Match      8.2%; Score 68; DB 7; Length 22;
Best Local Similarity 61.9%; Pred. No. 0.23;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      65 KCLKPKYSKISRYRHYCYSVYG 85
      ||:|:|:|:|:|:|:|:|:|
Db      1 KCIDFGSRIRRLRHYSDSVYG 21

RESULT 11
US-10-953-349-17182
; Sequence 17182, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17182
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Glycine max
; US-10-953-349-17182

```

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Query Match      7.8%; Score 65; DB 6; Length 369;
Best Local Similarity 23.2%; Pred. No. 9.9;
Matches 39; Conservative 24; Mismatches 59; Indels 54; Gaps 10;

Oy      1 MFODPQRPRLPOLCTELQTTIHDTLLCEVCKQOLL-----RRR- 41
Db      62 LKSPLSRP-----LFTAAEGGPEIYELLYSPDLLMKVDGQNRSLFNIAIMHROEKI 116

Oy      42 ---VYDF-APRDLCTIVVRDGNPVAVXOKLKFYSKI--SEVRNHCYSVYGTLLTEQQYN-- 93
Db      117 FNLIYDYGAMHDLTTSYRDNNNHHI-----LHLAKLAPSEQLHY--VSGAALOMORELL 169

Oy      94 -----KPLCDLLIRICINXOKPLCE-----EKORHLDKORPHNIRIGMTGRCNSCC 140
Db      170 WPKVEKVIQGLFPEIKDSQGRQTOMLFTEHNKLAEGE-----KMLKATYASC 219

```

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RESULT 12
US-10-953-349-6306
; Sequence 6306, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SOURCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6306
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6306

Query Match      7.7%; Score 63.5; DB 6; Length 419;
Best Local Similarity 21.0%; Pred. No. 16;
Matches 37; Conservative 19; Mismatches 69; Indels 51; Gaps 6;

QY    7 ERPRRLPOLCTELQTTIHDIILCEVCYCKQLLRREV-----YDFAPRD 49
DB    194 ESHKIPNVSVSITTHPIIAPKVHVAAYENKRKTENOKTSYSITVOGVNADGIFTD 253
QY    50 LCIIVRDNPPYAAXDKLKFYSKISEVRHYCYSYVGTTLEQQYNKPLCDLLIRCLNXKP 109
DB    254 VCI-----GNPSLITDDQDLLEKSSLSRGRARAGMLRDSWIVGSGEPLTDYL----- 300
QY    110 LCPEEKQ-----RHLDKKQ-----REHNIRGRMTRGRCMSCCRSSRTRENO 150
DB    301 LVPTTROMLTWTQHAFNESIGEIGIATPAFERLKRW-----ACLQRRIIVKIQ 350

RESULT 13
US-10-953-349-6305
; Sequence 6305, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SOURCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6305
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6305

Query Match      7.7%; Score 63.5; DB 6; Length 515;
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Search completed: June 6, 2006, 12:33:23
Job time : 11.9157 secs

Search completed: June 6, 2006, 12:33:23
Job time : 11.9157 secs

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OM protein - protein search, using sw model

Run on: June 6, 2006, 12:05:01 ; Search time 29.1084 Seconds

(without alignments)
499.124 Million cell updates/sec

Title: US-10-530-253-13

Perfect score: 830
Sequence: 1 MFQDPQPRPKLTPLCTELQ.....WTGRCMSCCRSSRTRETQL 151

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	99.2	158	1	protein E6 - human
2	578	69.6	149	1	protein E6 - human
3	523	63.0	149	1	protein E6 - human
4	520	62.7	149	1	protein E6 - human
5	496	59.8	149	1	protein E6 - human
6	487	58.7	148	2	protein E6 - human
7	487	58.7	148	2	protein E6 - human
8	484	58.3	148	2	protein E6 - human
9	460	55.4	151	1	protein E6 - human
10	459.5	55.4	158	2	protein E6 - human
11	455.5	54.9	158	1	protein E6 - human
12	451.5	54.4	158	1	protein E6 - human
13	449.5	54.2	158	1	protein E6 - human
14	438	52.8	191	1	protein E6 - human
15	436.5	52.6	150	2	protein E6 - human
16	426.5	51.4	155	1	protein E6 - human
17	385.5	46.4	153	2	protein E6 - human
18	379	45.7	154	2	protein E6 - human
19	372.5	44.9	155	2	protein E6 - human
20	366.5	43.3	155	1	protein E6 - human
21	304	36.6	150	1	protein E6 - human
22	303	36.5	153	1	protein E6 - human
23	301	36.3	150	1	protein E6 - human
24	297.5	35.8	159	1	protein E6 - human
25	294	35.4	150	1	protein E6 - human
26	292	35.2	159	2	protein E6 - human
27	290.5	35.0	154	2	protein E6 - human
28	288.5	34.8	154	2	protein E6 - human
29	288	34.7	150	1	protein E6 - human

30	283	34.1	142	2	protein E6 - human
31	273	32.9	150	1	protein E6 - human
32	268	32.3	150	1	protein E6 - human
33	239	28.8	148	2	protein E6 - human
34	231	27.8	152	2	protein E6 - human
35	154	18.6	138	2	protein E6 - human
36	143.5	17.3	141	2	protein E6 - human
37	137	16.5	156	1	protein E6 - human
38	136.5	16.4	140	1	protein E6 - human
39	134.5	16.2	139	1	protein E6 - human
40	132	15.9	161	2	protein E6 - human
41	129.5	15.6	207	2	protein E6 - human
42	128.5	15.5	141	2	protein E6 - human
43	127	15.3	57	2	protein E6 - human
44	127	15.3	273	1	protein E6 - human
45	123	14.8	157	2	protein E6 - human

ALIGNMENTS

RESULT 1

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Roweckamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A23355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SSE>

A:Cross-references: UNIPROT:P03126; UNIPARC:UPI000000138B; GB:K02718; NID:G333031; PIDN:AAAA6939.1; PT

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: UNIPARC:UPI000000138B; EMBL:K02718; NID:G333031; PIDN:AAAA6939.1; PT

C:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 99.2% ; Score 823; DB 1; Length 158;
Best Local Similarity 98.0% ; Pred. No. 2.7e-71;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	MFQDPQPRPKLTPLCTELQTTTHDITLLECYCKQQLLRREVDPAFDDICTVTRDGNPY	60
DB	8	MFQDPQPRPKLTPLCTELQTTTHDITLLECYCKQQLLRREVDPAFDDICTVTRDGNPY	67
QY	61	AVVQKCLKPKYSKISEYHYGVYGTLEQVYKPLCDLLIRCTNXPICPEKORHLD	120
DB	68	AVVQKCLKPKYSKISEYHYGVYGTLEQVYKPLCDLLIRCTNXPICPEKORHLD	127
QY	121	KKQRFNIRGRWTGRCMSCCRSSRTRETQL	151
DB	128	KKQRFNIRGRWTGRCMSCCRSSRTRETQL	158

RESULT 2

protein E6 - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: E40824; S36521
R/Marich, J.E.; Pontier, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A/Title: The phylogenetic relationship and complete nucleotide sequence of human papilloma-
A/Reference number: A40824; MUID:92124753; PMID:1310198
A/Accession: E40824
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-149 <MAR>
A/Cross-references: UNIPROT:P27228; UNIPARC:UPI00001383CF; GB:M74117; NID:G333050; PIDN:
R:Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36521
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-149
A/Cross-references: UNIPARC:UPI00001383CF; EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PI
A/Experimental source: Strain 35H
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F/30-66/Region: zinc finger CCCC motif
F/103-139/Region: zinc finger CCCC motif

Query Match 69.6%; Score 578; DB 1; Length 149;
Best Local Similarity 71.5%; Pred. No. 5.7e-48;
Matches 108; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTIYRDGNPY 60
Db 1 MFODPARPRYKHLCLNEVESHIEICLNCYCKQQLRSEVYDFACDLCTIYRREGPY 60
QY 61 AYXDKCLKFSKISEYRHYCYSVYGTLEQYKPLCDLIRICINXOKPLCPBEKQRHLD 120
Db 61 GVCKCLKFSKISEYRHYCYSVYGTLEQYKPLCDLIRICITCQKPLCPBEKQRHLE 120
QY 121 KQRFNIRGRWTRGCMSCCRSSRTRETQL 151
Db 121 EKKRFNIRGRWTRGCMSCWRP--TRRETEV 149

RESULT 3

W6WL31
E6 protein - human papillomavirus type 31
C/Species: human papillomavirus type 31
A/Note: host Homo sapiens (man)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: A32444
R/Goldborough, M.D.; Dislyvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A/Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-asso-
A/Reference number: A94398; MUID:89299478; PMID:2545036
A/Accession: A32444
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-149 <GOL>
A/Cross-references: UNIPROT:P17386; UNIPARC:UPI00001383CB; GB:J04353; NID:G333048; PIDN:
C/Comment: This protein may be involved in the oncogenic potential of this virus.
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F/30-66/Region: zinc finger CCCC motif
F/103-139/Region: zinc finger CCCC motif

Query Match 63.0%; Score 523; DB 1; Length 149;
Best Local Similarity 64.9%; Pred. No. 9.9e-43;
Matches 98; Conservative 18; Mismatches 33; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTIYRDGNPY 60
Db 1 MFKNPARPRKTLHLSALRIPYDELRLNLCYCKGQLTETELVDFAFDTLTIYVRDDTPH 60

QY 61 AYXDKCLKFSKISEYRHYCYSVYGTLEQYKPLCDLIRICINXOKPLCPBEKQRHLD 120
Db 61 GVCKCLKFSKISEYRHYCYSVYGTLEQYKPLCDLIRICITCQKPLCPBEKQRHLD 120
QY 121 KQRFNIRGRWTRGCMSCCRSSRTRETQL 151
Db 121 KKKRFNIRGRWTRGRCACWR--RPRRETQV 149

RESULT 4

W6WL33
E6 protein - human papillomavirus type 33
C/Species: human papillomavirus type 33
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C/Accession: A03683
R/Cole, S.T.; Strecek, R.E.
J. Virol. 58, 991-995, 1986
A/Title: Genome organization and nucleotide sequence of human papillomavirus type 33, whi
A/Reference number: A93020; MUID:86200464; PMID:3009902
A/Accession: A03683
A/Molecule type: DNA
A/Residues: 1-149 <COL>
A/Cross-references: UNIPROT:P06427; UNIPARC:UPI00001383CD; GB:M12732; NID:G333049; PIDN:
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F/30-66/Region: zinc finger CCCC motif
F/103-139/Region: zinc finger CCCC motif

Query Match 62.7%; Score 520; DB 1; Length 149;
Best Local Similarity 63.6%; Pred. No. 1.9e-42;
Matches 96; Conservative 19; Mismatches 34; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTIYRDGNPY 60
Db 1 MFQTEKRPRLHDLCOALETTHNIEIQVCECKPLQSEVYDFAFADLTIVYREGNPF 60
QY 61 AYXDKCLKFSKISEYRHYCYSVYGTLEQYKPLCDLIRICINXOKPLCPBEKQRHLD 120
Db 61 GICLCLKFSKISEYRHYCYSVYGTLEQYKPLCDLIRICITCQKPLCPBEKQRHLD 120
QY 121 KQRFNIRGRWTRGCMSCCRSSRTRETQL 151
Db 121 LNKRFNIRGRWTRGRCACWR--RRRETAL 149

RESULT 5

W6WL58
E6 protein - human papillomavirus type 58
C/Species: human papillomavirus type 58
A/Note: host Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: E36779
R/Kitil, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A/Title: Human papillomavirus type 58 DNA sequence.
A/Reference number: A36779; MUID:92024102; PMID:1656594
A/Accession: E36779
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-149 <KIR>
A/Cross-references: UNIPROT:P2655; UNIPARC:UPI00000081B; GB:D90400; NID:G222386; PIDN:
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F/30-66/Region: zinc finger CCCC motif
F/103-139/Region: zinc finger CCCC motif

Query Match 59.8%; Score 496; DB 1; Length 149;
Best Local Similarity 61.6%; Pred. No. 3.7e-40;
Matches 93; Conservative 20; Mismatches 36; Indels 2; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTIHDIIECVYCKQQLLRREYDFAFRDLCTIYRDGNPY 60
Db 1 MFQDAEKPRTLHDLCOALETSVHIEILKCECKKTLQSEVYDFAFADLTIVYRDGNPF 60

```

Oy      61  IVDDKCLKFYSKISBYRHVYCSVYGTTLDEQYNNKPLCDLLIRLNQXKPLCPKORHLD 120
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      61  AVCVKCTLRLLKISIEYRHVYNSLYGDTLEQTLKCLNELIRCIICORPLCPQEKKHVD 120
          |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||:

Oy      121 KQORFHHNIRGWTGRCMSCCRSSRTBRETEL 151
          :|||:|||:|||:|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      121 LNKRFHHNISGRWTRGCAVCMRP--RRROTQV 149

RESULT 6
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C:Accession: A61237
R:Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahruachman, A.; Warza, U
Int. J. Cancer 48, 516-522, 1991
A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma
A:Reference number: A61237; MUID:91258022; PMID:1646174
A:Accession: A61237
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-148 <TAK>
A:Cross-references: UNIPARC:UPI0000178415
A:Superfamily: papillomavirus E6 protein

```

	Query Match	58.7%	Score 487;	DB 2;	Length 148;
	Best Local Similarity	61.7%	Pred. No. 2.6e-39;		
	Matches	87;	Conservative 19;	Mismatches 35;	Indels 0; Gaps 0.
QY	1 MFODPQEPRRLPOLCTELQTTHIIILECYVCKOOLRREVEYDAFRDLCAIVRDGMPY	60			
Dd	1 MFDPPATPRRLHETCEVLSESVNHRIQCVCCKEQLREVEYKFLFDDLRIVYDNNPY	60			
QY	61 AVXDCKLFYSKISERYHYCYSVYGTLLIEQYNKECDLILRCINXQRPCEEKORHL	120			
Dd	61 GVCIMCLRFSLSKISERYHYQSVLYGKTLEERVRKSLTEITIRCIICQPLDCBEKERAYN	120			
QY	121 KQRRPHNRGRWTGCMSCCR	141			
Dd	121 AKKRPHNIMGRTGCSCEWR	141			

RESULT 7
S36573
E6 protein - human papillomavirus type 52
C/Species: human papillomavirus type 52
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36573
R/Dellus, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36573
A/Molecule type: DNA
A/Residues: 1-148
A/Cross-references: UNIPROT:P36814; UNIPARC:UPI00001383DD; EMBL:X74481; NTD:g397038; PDB:1Y83
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

[illegible]

```

QY      121 KKQRFHNRGRWTGRCMSCCR 141
          :|||||
Db      121 ANKRFHNRGRWTGRCSECCWR 141

```

RESULT 8
S36515
E6 protein - human papillomavirus type 34
C:Species: human papillomavirus type 34
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2009
C:Accession: S36515

submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36515
A:Molecule type: DNA
A:Residues: 1-148
A:Cross-references: UNIPROT:P36811, UNIPARC:UP100001383CE, EMBL:X74476, NID:g336989; PID
C:Superfamily: Papillomavirus E6 protein
Keywords: DNA binding; early protein; nucleus; zinc finger

[illegible]

```

RESULT 9
M6WL51
B6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E40415
R:Langui, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 51
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: E40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LIn>
A:Cross-references: UNIPROT:P26554; UNIPARC:UPI00001383DC; GB:M62877
C:Superfamily: papillomavirus B6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:/30-66/Region: zinc finger CCCC motif
F:/103-139/Region: zinc finger CCCC motif

```

Query Match	55.4%	Score 460;	DB 1;	Length 151;
Best Local Similarity	57.0%;	Pred. No. 1e-36;		
Matches	86;	Conservative 24;	Mismatches 41;	Indels 0; Gaps 0;
Qy	1	MFODPOBRPKLTCTELQTTHIDILLECVCYKQOGLRRVYFAFRLDCIYYRDGPNY	60	
		: : : : : :		
Dd	1	MEEDKRPRPTLHELCEALWMSHNNIOVVCCYCKEELCRADVVAATETIIVTRDNNPY	60	
Qy	61	AVXDKCLFYFSKISSEVHYHCYSVYGTLLEOOYNKPLCDLLIRCIINKOKPLCPPEEKORHL	120	
		:		
Dd	61	AVCKQCCLLFPSKIREVRYRSRVYGTLLLEIKTSKYLDLSIRCHRCGRPLGPBEKKQLVD	120	
		:		
Qy	121	KKQRFHNIRGRWTGRCMSCCRSSRTRETOL	151	

Db 121 EKKRFHEIAGKWTGQCANCWQRTQQRNETOV 151

RESULT 10

E6 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36561
R:Deilus, H.; Hofmann, B.
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469

A:Accession: S36561
A:Molecule type: DNA
A:Residues: 1-158
A:Cross-references: UNIPROT:P21735, UNIPARC:UPI00001383D8, EMBL:X74479, NID:g397022, PID
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 55.4%; Score 459.5; DB 2; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.2e-36;
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

2 FQDPERPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDPAFRDLCTVYRDGNPYA 61

4 FDDPKQRPYKLPDLCTELNTSLQDVSIACVCKATLEKTEVYQFAFKDLCTVYRDCIAYA 63

62 VXDCKLFKYSKISEYRHVCYVGTTLQOYNKPLCDLLIRICINXQKPLCPCEKQRLDK 121

64 ACHKCIDFYSRIRRLRYNSVGTLEKINTLEYNLLIRCLRCQKPLNPAEKRLHLD 123

Qy 122 KQRFNIRGRMTGRCMSCCSS-----RTRETOL 151

124 KRPFHNIAGYRGQCNCQDARQERLRRRETQV 158

RESULT 11

E6 protein - human papillomavirus type 18

C:Species: human papillomavirus type 18
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C/Accession: A26165; G26251
R:Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A>Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: A26165

A:Molecule type: DNA
A:Residues: 1-158 <SNE>
A:Cross-references: UNIPROT:P06463, UNIPARC:UPI000002C0FB, GB:X04773; NID:g60876; PIDN:C
R:Coie, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987

A>Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1
A:Reference number: A92937; MUID:87283882; PMID:3039146
A:Accession: G26251

A:Molecule type: DNA
A:Residues: 1-158 <COL>
A:Cross-references: UNIPARC:UPI00002C0FB, GB:X05015; NID:g60975; PIDN:CA28664.1; PID:G
R:MacLashewski, G.; Banks, L.; Wu-liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986

A>Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A:Reference number: A92791; MUID:86306665; PMID:3018129
A:Contents: annotation; identification of the protein
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 54.9%; Score 455.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 2.8e-36;
Matches 87; Conservative 21; Mismatches 42; Indels 5; Gaps 1;

Qy 2 FQDPERPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDPAFRDLCTVYRDGNPYA 61

Db 4 FEDPRRPYKLPDLCTELNTSLQDVSIACVCKATLEKTEVYQFAFKDLCTVYRDCIAYA 63

Qy 62 VXDCKLFKYSKISEYRHVCYVGTTLQOYNKPLCDLLIRICINXQKPLCPCEKQRLDK 121

Db 64 ACHKCIDFYSRIRRLRYNSVGTLEKINTLEYNLLIRCLRCQKPLNPAEKRLHLD 123

Qy 122 KQRFNIRGRMTGRCMSCCSSR-----TRRETOL 151

Db 124 KRPFHNIAGYRGQCNCQDARQERLRRRETQV 158

RESULT 12

E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180
A>Note: host Homo sapiens (man)
C/Accession: C40509
R:Reuter, S.; Deilus, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991

A>Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509

A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P27962; UNIPARC:UPI00000082F; GB:M73258
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger

F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 54.4%; Score 451.5; DB 1; Length 158;
Best Local Similarity 55.1%; Pred. No. 6.8e-36;
Matches 86; Conservative 21; Mismatches 44; Indels 5; Gaps 1;

Qy 1 MFQDPERPKLPOLCTELQTTIHDIILECVYCKQQLRREYVDPAFRDLCTVYRDGNPY 60

Db 3 LFHNPERRPYKLPDLCTELTTHDVTIDVYCRQLQRTVEYFAFGDLNVVYRDGVPL 62

Qy 61 AYXDKCLFKYSKISEYRHVCYVGTTLQOYNKPLCDLLIRICINXQKPLCPCEKQRLDK 120

Db 63 AACOSCKIFYAKRLRLRYNSVGTLEKINTLEYNLLIRCLRCQKPLNPAEKRLHLD 122

Qy 121 KQRFNIRGRMTGRCMSCCSS-----RTRETOL 151

Db 123 SKRPFHNIAGNFTGQCNCQDARQERLRRRETQV 158

RESULT 13

E6 protein - human papillomavirus type 39

C:Species: human papillomavirus type 39
A>Note: host Homo sapiens (man)
C/Accession: A38502
R:Volpers, C.; Strecek, R.E.
Virology 181, 419-423, 1991

A>Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; MUID:91135017; PMID:1847266
A:Accession: A38502

A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <VOL>
A:Cross-references: UNIPROT:P24835; UNIPARC:UPI00001383D2; GB:M62849; EMBL:M38185; NID:g
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif


```

Query Match      54.2%; Score 449.5; DB 1; Length 158;
Best Local Similarity 55.5%; Pred. No. 1.1e-35;
Matches 86; Conservative 19; Mismatches 45; Indels 5; Gaps 1;

QY 2 FQDEQERBRKLPOLCTELQTTIHDLIECVCKQOOLREYVYDFAFRDLCTIVRSGNRYA 61
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 4 FHNPAERYRKLPLDCTTLDITLQDITIAQVCRRLQOTLEYEYEFASDLYVYVNRGEPLA 63
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 62 VXDCKLRYSKLSIEFRHYCYVGTTLLEQOYNKPLCDLLIRICINAKQLCPBEKORHDK 121
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 64 ACOSCIKRYAKIRREIRYVSDSVYATTLLENITNTKLYNNLLIRCMCLKPLCPAEKLRHNS 123
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY 122 KQRFHNIRGRWTRCMSCCRSSR-----TRRETOL 151
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 124 KRREHKTAGSYTGQCRRCRCWTTKREDRRLTRRETQV 158
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

```

RESULT 14
W6WLR1 E6 protein - rheus papillomavirus (type 1)
C:Species: rheus papillomavirus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38503
R:Ostrow, R.S.; Labreesh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A:Title: Characterization of the complete Rhv1 genomic sequence and an integration loop
A:Reference number: A38503; PMID:91135018; PMID:1847267
A:Accession: A38503
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-191 <OST>
A:Cross-references: UNIPROT:P22159; UNIPARC:UP100001383EE; EMBL:M37717
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:60-96/Region: zinc finger CCCC motif
F:133-169/Region: zinc finger CCCC motif

[illegible]

RESULT 15

S36544
E6 protein - human papillomavirus type 26
C:Species: human papillomavirus type 26
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36544
R:Dellus, H., Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36544
A:Molecule type: DNA
A:Residues: 1-150
A:Cross-references: UNIPROT:P36807, UNIPARC:UPI00001383C5, EMBL:X74472, NTD:g396956, PIRSD:
C:Superfamily: papillomavirus E6 protein
C:Keywords: early protein; zinc finger

Query Match	52.6%;	Score 436.5;	DB 2;	Length 150;
Best Local Similarity	55.0%;	Pred. NO. 1.7e-34;		

[illegible]

Search completed: June 6, 2006, 12:11:55
Job time : 30.1084 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:34 ; Search time 232.867 Seconds
(without alignments)
599.815 Million cell updates/sec

Title: US-10-530-253-13
Perfect score: 830
Sequence: 1 MFQDPQRPRLKLPOLCTELQ.....WTGRCMSCCRSSRTRETQL 151

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	826	99.5	151	2	Q77JC7 HPV16
2	826	99.5	151	2	Q89852 HPV16
3	826	99.5	151	2	Q89852 HPV16
4	824	99.3	151	2	Q89852 HPV16
5	823	99.2	151	2	Q89852 HPV16
6	823	99.2	151	2	Q89852 HPV16
7	823	99.2	151	2	Q89852 HPV16
8	823	99.2	151	2	Q89852 HPV16
9	823	99.2	151	2	Q89852 HPV16
10	823	99.2	151	2	Q89852 HPV16
11	821	98.9	151	2	Q89852 HPV16
12	821	98.9	151	2	Q89852 HPV16
13	820	98.8	151	2	Q89852 HPV16
14	820	98.8	151	2	Q89852 HPV16
15	819	98.7	151	2	Q89852 HPV16
16	819	98.7	151	2	Q89852 HPV16
17	819	98.7	151	2	Q89852 HPV16
18	819	98.7	151	2	Q89852 HPV16
19	819	98.7	151	2	Q89852 HPV16
20	819	98.7	151	2	Q89852 HPV16
21	818	98.6	151	2	Q89852 HPV16
22	818	98.6	151	2	Q89852 HPV16
23	817	98.4	151	2	Q89852 HPV16
24	817	98.4	151	2	Q89852 HPV16
25	817	98.4	151	2	Q89852 HPV16
26	816	98.3	151	2	Q89852 HPV16
27	816	98.3	151	2	Q89852 HPV16
28	816	98.3	151	2	Q89852 HPV16
29	815	98.2	151	2	Q89852 HPV16
30	815	98.2	151	2	Q89852 HPV16
31	814	98.1	151	2	Q89852 HPV16

32	814	98.1	158	2	Q9QDH3 HPV16	Q9QDH3 human papill
33	814	98.1	161	2	Q919B1 HPV16	Q919B1 human papill
34	813	98.0	158	2	Q8QRE1 HPV16	Q8QRE1 human papill
35	812	97.8	151	2	Q12335 HPV16	Q12335 human papill
36	811	97.7	151	2	Q9WMP4 HPV16	Q9WMP4 human papill
37	810	97.6	151	2	Q12336 HPV16	Q12336 human papill
38	809	97.5	158	2	Q8QDH7 HPV16	Q8QDH7 human papill
39	808	97.3	151	2	Q8B821 HPV16	Q8B821 human papill
40	808	97.3	151	2	Q9WMP2 HPV16	Q9WMP2 human papill
41	808	97.3	161	2	Q919A9 HPV16	Q919A9 human papill
42	806	97.1	151	2	Q76TS0 HPV16	Q76TS0 human papill
43	806	97.1	151	2	Q80966 HPV16	Q80966 human papill
44	806	97.1	158	2	Q8JMU8 HPV16	Q8JMU8 human papill
45	804	96.9	151	2	Q77E16 HPV16	Q77E16 human papill

ALIGNMENTS

RESULT 1
Q77JC7 HPV16 PRELIMINARY; PRT; 151 AA.
ID Q77JC7;
AC Q77JC7;
DT 05-JUN-2004, integrated into UniprotKB/TREMBL.
DT 05-JUN-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Xinjiang.
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang O., Zhang F.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
RT Biopsies in Xinjiang."
RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA van duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RX MEDLINE=20112892; PubMed=10644829;
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis."
RL J. Gen. Virol. 81:317-325(2000).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=2242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RX Deillipis V.R., Ayala F.U., Villareal L.P.;
RA "Evidence of diversifying selection in human papillomavirus type 16 E6
RT but not E7 oncogene."
RL J. Mol. Evol. 55:491-499(2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Cruz M., Cergueta D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RX Martins C.R.F.;
RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RA Cruz M.R., Martins C.R.F.;
RX Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; AF37851; AAG5940.1; -; Genomic DNA.
CC EMBL; AJ388057; CAB45106.1; -; Genomic DNA.
CC EMBL; AJ388059; CAB45106.1; -; Genomic DNA.
CC EMBL; AY089951; AAM11875.1; -; Genomic DNA.
CC EMBL; AY089954; AAM11881.1; -; Genomic DNA.
CC EMBL; AY112663; AAM51854.1; -; Genomic DNA.
CC GO; GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query March 99.5%; Score 826; DB 2; Length 151;
Best Local Similarity 98.7%; Pred. No. 2.4e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60

QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLRCINXOKPLCPBEKQRHLD 120
DB 61 AVCDKCLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLRCINXOKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151
DB 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151

RESULT 2

Q89852_9PAPI PRELIMINARY; PRT; 151 AA.
AC Q89852_9PAPI

DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 1.

DE Early transforming protein E6.

OS Human papillomavirus.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.

NCBI TaxID=10566;

[1]

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=9607021; PubMed=7494284;

RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,

RA Jensen S.A.;

RT "Human papillomavirus type 16 variant lineages in United States

RT populations characterized by nucleotide sequence analysis of the E6,

RT L2, and L1 coding segments.";

RL J. Virol. 69:7743-7753(1995).

[2]

NP NUCLEOTIDE SEQUENCE.

RA Farmer A.D.;

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

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CC EMBL: U34134; AAA91681.1; -; Genomic DNA.

DR EMBL: U34127; AAA91674.1; -; Genomic DNA.

DR EMBL: U34133; AAA91680.1; -; Genomic DNA.

DR GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query March 99.5%; Score 826; DB 2; Length 151;
Best Local Similarity 98.7%; Pred. No. 2.4e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60

QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLRCINXOKPLCPBEKQRHLD 120
DB 61 AVCDKCLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLRCINXOKPLCPBEKQRHLD 120

QY 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151

DB 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151

RESULT 3

Q9WH13_HPV16

ID Q9WH13_HPV16 PRELIMINARY; PRT; 158 AA.

AC Q9WH13_

DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.

DT 07-FEB-2006, entry version 1.

DE E6.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Alphapapillomavirus.

NCBI TaxID=333760;

[1]

NP NUCLEOTIDE SEQUENCE.

RX MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9668;

RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;

RT "Establishment of the human papillomavirus type 16 (HPV-16) life cycle

RT in an immortalized human foreskin keratinocyte cell line.";

RL Virology 262:344-354(1999).

[2]

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=E-C109G;

RX MEDLINE=22182962; PubMed=12195358; DOI=10.1006/342048;

RA Chan P.K.S., Lam C.W., Chung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

RA Cheung J.L.K., Xu L.Y., Cheng A.F.;

RT "Human papillomavirus type 16 intertypic variant infection and risk

RT for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).

[3]

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=QV16936E;

RX PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;

RA Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;

RT "Diversifying selection in human papillomavirus type 16 lineages based

RT on complete genome analyses.";

RL J. Virol. 79:7014-7023(2005).

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CC EMBL: AF125673; AAD33252.1; -; Genomic DNA.

DR EMBL: AF486322; AAL96627.1; -; Genomic DNA.

DR EMBL: AY686580; AAV91652.1; -; Genomic DNA.

DR GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

SQ SEQUENCE 158 AA; 19173 MW; 9F0CF5ADDA2ED7FE CRC64;

Query March 99.5%; Score 826; DB 2; Length 158;
Best Local Similarity 98.7%; Pred. No. 2.5e-73;
Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 60
DB 8 MFQDPQERPRKLPOLCTELQTTIHDIIECYCKQQLLRREYDPAFRDLCTVYRDGNY 67

QY 61 AVXDKLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLRCINXOKPLCPBEKQRHLD 120
DB 68 AVCDKCLKFSKISEYHYHCYSVGTLEQOYNKPLCDLLRCINXOKPLCPBEKQRHLD 127

QY 121 KKQRFHNIRGRWTCRSCSSSRTRETOL 151
DB 128 KKQRFHNIRGRWTCRSCSSSRTRETOL 158

RESULT 4
Q9WMP5_HPV16 PRELIMINARY; PRT; 151 AA.
ID Q9WMP5_HPV16

AC Q9MWP5; integrated into UniProtKB/TrEMBL.
 DT 01-NOV-1999, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=333760;
 OX (1)
 RP NCULEOTIDE SEQUENCE.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaasen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Weljor C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis";
 RL J. Gen. Virol. 81:317-325(2000).
 RN (2)
 RP NCULEOTIDE SEQUENCE.
 RA Duin M.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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 CC CC
 EMBL: AJ242681; CAB45381.1; -; Genomic DNA.
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 QO SEQUENCE 151 AA; 18320 MW; 617D2D5FD93F8917 CRC64;

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Query March 99.3%; Score 824; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 3,8e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQSEPRKLPQLCTELQTTIHIIIECYCKQOQLRREYVDPAFBDLCVYRDGMPY 60
Db 1 MFODPQSEPRKLPQLCTELQTTIHIIIECYCKQOQLRREYVDPAFBDLCVYRDGMPY 60
QY 61 AVXDCKLKFYSKISEYRHYCYSVYGTLLIQYNNKPLCDLLIRCIHXORPLCEEKQRLD 120
Db 61 AVCDCKLKFYSKISEYRHYCYSVYGTLLIQYNNKPLCDLLIRCIHQCPPLCEEKQRLD 120
QY 121 KKQRFHNRGRWGTGRWCSCCSSRRRETQL 151
Db 121 KKQRFHNRGRWGTGRWCSCCSSRRRETQL 151

RESULT 5
Q77816.HPV16
ID Q77816.HPV16 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxId=333760;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=2011892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RT J. Gen. Virol. 81:317-325 (2000).
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DR EMBL; AJ388056; CAB45104.1; -; Genomic DNA.
DR EMBL; AJ388061; CAB45114.1; -; Genomic DNA.
DR EMBL; AJ388066; CAB45124.1; -; Genomic DNA.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
SQ SEQUENCE 151 AA; 18334 MW; F9F92A2FCBBA6C02 CRC64;

```

Query Match      99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4.7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0

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Qy	1	MEQDQDSEPRKLPOLCTELQTTIHIIIEECYCKOOLLAREVYDPAEPLCTVIRGNGNY	60
Db	1	MFQDQDSEPRKLPOLCTELQTTIHIIIEECYCKOOLLAREVYDPAEPLCTVIRGNGNY	60
Qy	61	AVDCKLKFYSKISISYRHYCVSVGTTLLBOQYNKPLCDLLRCINQKPLCPBEKORHLD	120
Db	61	AVDCKLKFYSKISISYRHYCVSVGTTLLBOQYNKPLCDLLRCINQKPLCPBEKORHLD	120
Qy	121	KKQRFHNIIRGWTGRCMCCRRSRRTRRETOL	151
Db	121	KKQRFHNIIRGWTGRCMCCRRSRRTRRETOL	151

RESULT 6
089755 9PAPI

ID Q89755_9PAPI PRELIMINARY; PRT; 151 AA.
AC Q89755;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 24.
DE Early transforming protein E6.
DE Human Papillomavirus.
OS
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
OX NCBI_TaxId=10566;
RX
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
J. Virol. 69:7743-7753 (1995).
RL

RP NUCLEOTIDE SEQUENCE.
 RA Farmer A.D.¹
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL; U34126; AAA91673.1; -; Genomic DNA.
 DR EMBL; U34111; AAA91658.1; -; Genomic DNA.
 DR EMBL; U34121; AAA91668.1; -; Genomic DNA.
 DR EMBL; U34123; AAA91670.1; -; Genomic DNA.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; B6; 1.
 DR SEQUENCE 151 AA; 18334 MW; F8F82A2FC6BA6C02 CRC64;

Query Match	99.2%	Score 823;	DB 2;	length 151;
Best Local Similarity	98.0%	Pred. No. 4.7e-73;		
Matches 148;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0

Qy 1 MFODPOEPRKLPOLCTEIQTTHDIIEECVCKQOLLREVDPAFRDLCTIYVRDGNPY 60

Db 1 MFODPOEPRKLPOLCTEIQTTHDIIEECVCKQOLLREVDPAFRDLCTIYVRDGNPY 60

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Qy 61 AVXDCKLFYSKISEYRHVYCYVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Db 61 AVCDCKLFYSKISEYRHVYCYVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Qy 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 7
Q8BB20 HPV16 PRELIMINARY; PRT; 151 AA.
ID Q8BB20 HPV16
AC Q8BB20
DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Deillipis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
but not E7 oncogenes."
RL J. Mol. Evol. 55:491-499(2002).
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CC -----
DR EMBL: AY089953; AAM1879.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR SEQUENCE 151 AA; 18319 MW; 7C8D23EFCF4F8C17 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 4,7e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
Db 1 MFQDPQERPRKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
Qy 61 AVXDCKLFYSKISEYRHVYCYVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Db 61 AVCDCKLFYSKISEYRHVYCYVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Qy 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151
Db 121 KKORFHNIRGWTGRCMSCCRSSRTRETOL 151

RESULT 8
VE6_HPV16 STANDARD; PRT; 158 AA.
ID VE6_HPV16
AC P03126; Q71B17;
DT 21-JUL-1986, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1986, sequence version 1.
DT 07-MAR-2006, entry version 45.
DE Protein E6.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RP MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Roweckamp W.G.;
```

```
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RC STRAIN=Isolate European German 131;
RA Terai M., Fu L., Ma Z., Burk R.D.;
RT "Cloning and sequencing of non-European human papillomavirus (HPV)
variant complete genomes from cervicovaginal cells by an overlapping
PCR method."
RT Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
RL [3]
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA) OF 31-50.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Behau-Arnaudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia."
RL J. Gen. Virol. 71:809-817(1990).
RN [4]
RP INTERACTION WITH HUMAN FBIN1, AND INHIBITION OF E6-MEDIATED
RP TRANSFORMATION.
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.U.;
RT "Interaction of oncogenic Papillomavirus E6 proteins with fibulin-1."
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -1- FUNCTION: Transcriptional transactivator. Binds double stranded
CC DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-
CC protein ligase, the human TP53/p53 tumor suppressor protein by
CC targeting it to degradation. Binds and targets human MDM2/MDP2
CC protein to degradation. Those two functions presumably contribute
CC to transforming activity (By similarity). Interaction with human
CC FBIN1 protein also seems to be linked to cell transformation.
CC -1- SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which
CC interacts with human p53. Binds to human FBIN1 and MDP2 (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -1- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more
CC often associated with malignant genital cancers in humans.
CC -1- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
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CC -----
DR EMBL: K02718; AAA46939.1; -; Genomic DNA.
DR EMBL: AF536179; AA010712.1; -; Genomic DNA.
DR EMBL: D00735; BA00632.1; -; Genomic DNA.
DR PIR: A03682; W6WHS.
DR PDB: 2FK4; NMR; A=87-158.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
DR 3D-structure: Activator: DNA-binding; Early protein; Metal-binding;
KW Nuclear protein; Oncogene; Transcription; Transcription regulation;
KW Zinc; Zinc-finger.
FT CHAIN 1 158
FT FTID=PRO_000013336.
FT ZN_FING 37 73
FT ZN_FING 110 146
FT MOTIF 155 158
FT MOTIF 17 17
FT CONFLICT 90 90 L -> V (in Ref. 2).
FT CONFLICT 90 90 L -> V (in Ref. 2).
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFB37EB CRC64;

Query Match 99.2%; Score 823; DB 1; Length 158;
Best Local Similarity 98.0%; Pred. No. 4,9e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFQDPQERPRKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 60
Db 8 MFQDPQERPRKLPOLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCTIYRDGPNY 67
Qy 61 AVXDCKLFYSKISEYRHVYCYVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 120
Db 61 AVCDCKLFYSKISEYRHVYCYVYGTTLLEQYNNKPLCDLLIRCTINXQKPLCPBEKQRLD 127
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Qy 121 KGORFHNIRGRWTCRMSCCSSSRTRETOL 151
Db 128 KGORFHNIRGRWTCRMSCCSSSRTRETOL 158

RESULT 9
ID 054732 HPV16 PRELIMINARY; PRT: 158 AA.
AC 054732 HPV16, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DE 07-FEB-2006, entry version 5.
DE Transforming protein E6.
GN Name:E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=E-6, E-G187T, and E-G538T;
RC MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intracyclic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=QV17722E, and QV15521E;
RC PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA Chen Z., Terai M., Fu L., Herrero R., Desai R., Burk R.D.;
RT "Diversifying selection in human papillomavirus type 16 lineages based
RT on complete genome analyses.";
RL J. Virol. 79:7014-7023(2005).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Beb-102;
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.P.;
RT "Human papillomavirus type 16 variants in Central Brazil.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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CC
EMBL: AF486311; AAL96616.1; -; Genomic DNA.
EMBL: AY686584; AAV91684.1; -; Genomic DNA.
EMBL: AF486310; AAL96615.1; -; Genomic DNA.
EMBL: AF486312; AAL96617.1; -; Genomic DNA.
EMBL: AF486313; AAL96618.1; -; Genomic DNA.
EMBL: AF486317; AAL96622.1; -; Genomic DNA.
EMBL: AF486321; AAL96625.1; -; Genomic DNA.
EMBL: AF486321; AAL96626.1; -; Genomic DNA.
EMBL: AY089819; AAM29167.1; -; Genomic DNA.
EMBL: AY685819; AAV91660.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
SQ SEQUENCE 158 AA; 19187 MM; 01FEFSADCFD37EB CRC64;

Query Match 99.2%; Score 823; DB 2; Length 158;
Best Local Similarity 98.0%; Pred. No. 4.9e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 128 KGORFHNIRGRWTCRMSCCSSSRTRETOL 158

RESULT 10
ID 0519C6 HPV16 PRELIMINARY; PRT: 161 AA.
AC 0519C6 HPV16, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DE 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21846229; PubMed=11857370; DOI=10.1002/jic.10103;
RA Watts K.J., Thompson C.H., Cozzare Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
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CC
EMBL: AF404697; AAL01351.1; -; Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 161 AA; 19628 MM; 15D32F0F12E00460 CRC64;

Query Match 99.2%; Score 823; DB 2; Length 161;
Best Local Similarity 98.0%; Pred. No. 5e-73;
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MFOQPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGNPY 60
Db 11 MFOQPQERPRKLPOLCTELQTTIHDIIECYCKQQLRREVDPAFADLCIVRDGNPY 70

Qy 61 AVXKCLKFYKISRYRHYCVSVGTTLEQOYNKPLCDLLRCINXQKPLCPBEKQRHLD 120
Db 71 AVXKCLKFYKISRYRHYCVSVGTTLEQOYNKPLCDLLRCINXQKPLCPBEKQRHLD 130

Qy 121 KGORFHNIRGRWTCRMSCCSSSRTRETOL 151
Db 131 KGORFHNIRGRWTCRMSCCSSSRTRETOL 161

RESULT 11
ID 08B319 HPV16 PRELIMINARY; PRT: 151 AA.
AC 08B319 HPV16, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 1.
DE 07-FEB-2006, entry version 13.
DE Early transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=22424222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RA Defillipis V.R., Ayala F.J., Villareal L.B.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
RT but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
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CC	-----
DR	EMBL: AY089955; AAM1883.1; -; Genomic DNA.
DR	GO: GO:0042025; C:host cell nucleus; IEA.
DR	GO: GO:0003677; F:DNA binding; IEA.
DR	InterPro: IPR00134; E6.
DR	Pfam: PF00518; E6; 1.
SO	SEQUENCE 151 AA; 18319 MW; 6F9D2A2F5A5F88F7 CRC64;
Query Match	
Best Local Similarity 98.9%; Score 821; DB 2; Length 151;	
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
OY	1 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLCTIVRDGMPY 60
DB	1 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLCTIVRDGMPY 60
OY	61 AVXDCKLFYSKISISYRHYCVSVGTTLEQYNNKPLCDLLIRCNIXKQKPLCEBEQRHLD 120
DB	61 AVXDCKLFYSKISISYRHYCVSVGTTLEQYNNKPLCDLLIRCNIXKQKPLCEBEQRHLD 120
OY	121 KKQRFHNIRGRWTGRCMSCCRSSRRRETOL 151
DB	121 KKQRFHNIRGRWTGRCMSCCRSSRRRETOL 151
RESULT 12	
QAVRNS HPV16	
AC	QAVRNS HPV16 PRELIMINARY; PRT; 158 AA.
DT	05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT	05-JUL-2005, sequence version 1.
DT	07-FEB-2006, entry version 4.
DE	E6.
OC	Human papillomavirus type 16.
OC	Virusess; dsDNA virusess, no RNA stage; Papillomaviridae;
OC	Alphapapillomavirus.
OX	NCBI_TaxID=333760;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=QV18158E;
RX	PubMed15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
RA	Chen Z., Terai M., Fu L., Herrero R., Desalle R., Burk R.D.;
RT	"Diversifying selection in human papillomavirus type 16 lineages based
RT	on complete genome analyses.";
RL	J. Virol. 79:7014-7023(2005).
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DR	EMBL: AY686583; AAV91676.1; -; Genomic DNA.
DR	GO: GO:0042025; C:host cell nucleus; IEA.
DR	GO: GO:0003677; F:DNA binding; IEA.
SO	SEQUENCE 158 AA; 19172 MW; 91ECF5AD4CED31E CRC64;
Query Match	
Best Local Similarity 98.9%; Score 821; DB 2; Length 158;	
Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;	
OY	1 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLCTIVRDGMPY 60
DB	8 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLLRREYDPAFRLCTIVRDGMPY 67
OY	61 AVXDCKLFYSKISISYRHYCVSVGTTLEQYNNKPLCDLLIRCNIXKQKPLCEBEQRHLD 120
DB	68 AVXDCKLFYSKISISYRHYCVSVGTTLEQYNNKPLCDLLIRCNIXKQKPLCEBEQRHLD 127
OY	121 KKQRFHNIRGRWTGRCMSCCRSSRRRETOL 151
DB	128 KKQRFHNIRGRWTGRCMSCCRSSRRRETOL 158
RESULT 13	

OQ8RD7	HPV16	PRELIMINARY; PRF; 158 AA.
ID	OQ8RD7_HPVI6	
AC	OQ8RD7;	
DT	01-JUN-2002,	integrated into UniProtKB/TREMBL.
DT	01-JUN-2002,	sequence version 1.
DT	07-FEB-2006,	entry version 13.
DE	E6 protein.	
OS	Human papillomavirus type 16.	
OC	Virusae; dsDNA viruses, no RNA stage; Papillomaviridae;	
CC	Alphapapillomavirus.	
NX	NCBI_TaxId=333760;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=E-C44T;	
RX	MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;	
RA	Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,	
RA	Cheng J.L.K., Xu L.Y., Cheng A.F.;	
RT	"Human papillomavirus type 16 intraepithelial infection and risk	
RT	for cervical neoplasia in southern China."	
RL	J. Infect. Dis. 186:696-700(2002).	
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CC	-----	
DR	EMBL; AF468318; AAL96623.1; -; Genomic DNA.	
DR	GO; GO:0042025; C:host cell nucleus; IEA.	
DR	GO; GO:0003677; F:DNA binding; IEA.	
DR	InterPro; IPR001334; E6.	
DR	Pfam; PF00518; E6; 1.	
SQ	SEQUENCE 158 AA; 19173 MW; 14E8F5ADCFDB3640 CRC64;	
Query Match	98.8%; Score 820; DB 2; Length 158;	
Beet Local Similarity	97.4%; Pred. No. 9.8e-73;	
Matches 147; Conservative 2; Mismatches 0; Gaps 0;		
OY	1 MFQDPOERPRRLPOLCTELQTTTHIDILCEVYCCKOQLLRGVYDFAPRDLCTIYRGDNPY 60	
DB	8 MFQDPOERPRRLPOLCTELQTTTHIDILCEVYCCKOQLLRGVYDFAPRDLCTIYRGDNPY 67	
OY	61 AVHXKCLAFYSKISIEYHYHCYSVGTLEQOYNKPLCDLLIRLCINXOKPLCPBEKQRHLD 120	
DB	68 AVXCCKLAFYSKISIEYHYHCYSVGTLEQOYNKPLCDLLIRLCINXOKPLCPBEKQRHLD 127	
OY	121 KKQRFHNIRGRWTCRMSCCRSSSTRRETOL 151	
DB	128 KKQRFHNIRGRWTCRMSCCRSSSTRRETOL 158	
RESULT 14		
OQ8RD8	HPV16	PRELIMINARY; PRF; 158 AA.
ID	OQ8RD8_HPVI6	
AC	OQ8RD8;	
DT	01-JUN-2002,	integrated into UniProtKB/TREMBL.
DT	01-JUN-2002,	sequence version 1.
DT	07-FEB-2006,	entry version 13.
DE	E6 protein.	
OS	Human papillomavirus type 16.	
OC	Virusae; dsDNA viruses, no RNA stage; Papillomaviridae;	
CC	Alphapapillomavirus.	
OX	NCBI_TaxId=333760;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=E-G44T;	
RX	MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;	
RA	Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,	
RA	Cheng J.L.K., Xu L.Y., Cheng A.F.;	
RT	"Human papillomavirus type 16 intraepithelial infection and risk	
RT	for cervical neoplasia in southern China."	
RL	J. Infect. Dis. 186:696-700(2002).	
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DR EMBL: AF486316; AAL36621.1; -: Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19188 MW; 01FE5B1D21AF7EB CRC64;

Query Match 98.8%; Score 820; DB 2; Length 158;
Best Local Similarity 97.4%; Pred. No. 9.8e-73;
Matches 147; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 60
DB 8 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 67
QY 61 AVXDCKLFYSKISEYRHYSYVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 68 AVCDCKLFYSKISEYRHYSYVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 127
QY 121 KKORFHNIRGRWTCRSCSSRTRETOL 151
DB 128 KKORFHNIRGRWTCRSCSSRTRETOL 158

RESULT 15

077ZJ5 HPV16 PRELIMINARY; PRT; 151 AA.
AC 077ZJ5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: AF003019; AAB70736.1; -: Genomic DNA.
DR EMBL: AF003018; AAB70735.1; -: Genomic DNA.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18221 MW; 60CDD2A34DAF48CB7 CRC64;

Query Match 98.7%; Score 819; DB 2; Length 151;
Best Local Similarity 98.0%; Pred. No. 1.2e-72;
Matches 148; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 60
DB 1 MFODPQERPRKLPOLCTELQTTIHDIIECVYCKQQLRREYDPAFRDLCTIVRDGNY 60
QY 61 AVXDCKLFYSKISEYRHYSYVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
DB 61 AVCDCKLFYSKISEYRHYSYVGTTLBOQYNKPLCDLLIRICINXQKPLCPBEKQRHLD 120
QY 121 KKORFHNIRGRWTCRSCSSRTRETOL 151
DB 121 KKORFHNIRGRWTCRSCSSRTRETOL 151

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:15 ; Search time 143.655 Seconds
(without alignments)
311.909 Million cell updates/sec

Title: US-10-530-253-14

Sequence: 1 MHGDTPTLHEFMLDQPEPTT.....LEDLLMGTGLIVXPCSQKP 98

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

A_Geneseq_8:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

9: Geneseqp2005s:*

10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	99.4	248	8	AD044070 Amino aci
2	513	99.2	98	8	AED13079 HPV16 E7
3	513	99.2	220	2	AAV25378 HPV fusio
4	513	99.2	220	2	AAV02634
5	513	99.2	220	9	AED52640
6	513	99.2	248	8	AD044068
7	513	99.2	805	6	ADA27366
8	513	99.2	805	7	ADA92544 HPV-16 L2
9	513	99.2	805	7	ADA14293
10	513	99.2	805	7	AAE38618
11	512	99.0	98	2	AAE22767 HPV E7 pe
12	512	99.0	98	2	AAE42361
13	512	99.0	98	2	AAW46886
14	512	99.0	98	3	AAV58474
15	512	99.0	98	3	AAV57721
16	512	99.0	98	4	AAV57721 Human pap
17	512	99.0	98	4	AAV57721 Human pap
18	512	99.0	98	4	AAV01718
19	512	99.0	98	4	AAV72607
20	512	99.0	98	4	AAE67546
21	512	99.0	98	4	AAE86332
22	512	99.0	98	5	AAU77713 Human pap
23	512	99.0	98	5	AAU10810
					Abb82375 Wild-type

24	512	99.0	98	5	AA016630	AA016630 Human pap
25	512	99.0	98	7	ADP09516	ADP09516 Human pap
26	512	99.0	98	7	ADP18632	ADP18632 Human pap
27	512	99.0	98	8	ADL90076	ADL90076 Human pap
28	512	99.0	98	8	ADM32916	ADM32916 Amino aci
29	512	99.0	98	8	AD044073	AD044073
30	512	99.0	98	8	ADN49005	ADN49005
31	512	99.0	98	8	ADU66362	ADU66362 Human pap
32	512	99.0	98	8	ADX15532	ADX15532 Human pap
33	512	99.0	98	9	ADY69083	ADY69083 HPV 16 E7
34	512	99.0	98	9	AEA40816	AEA40816 Ancl-apop
35	512	99.0	98	9	AEH11989	AEH11989 HPV16 E7
36	512	99.0	98	9	AEC96392	AEC96392 HPV prote
37	512	99.0	98	9	AEC98871	AEC98871 HPV 16 En
38	512	99.0	98	9	AED13078	AED13078 HPV16 E7
39	512	99.0	98	9	AED64360	AED64360 Human pap
40	512	99.0	98	10	AE894089	AE894089 HPV16 E7
41	512	99.0	99	9	AD088451	AD088451 HPV16 E7
42	512	99.0	99	9	ADY92615	ADY92615 HPV16 E7
43	512	99.0	121	4	AAE31608	AAE31608 Amino aci
44	512	99.0	198	4	AAE31616	AAE31616 Amino aci
45	512	99.0	212	8	ADT75831	ADT75831 Novel Fve

ALIGNMENTS

RESULT 1
AD044070
ID AD044070 standard; protein; 248 AA.
XX
AC AD044070;
XX
DT 15-JUL-2004 (first entry)
XX
DE Amino acid sequence of a fusion protein designated E7E6Pentm.
XX
KM E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer;
KM gene; ss.
XX
OS Human papillomavirus type 16.
OS Synthetic.
XX
PN WO2004030636-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003WO-US031726.
XX
PR 03-OCT-2002; 2002US-0415929P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Smith L, Cassecci MC;
XX
DR WPI; 2004-316328/29.
XX
N-PSDB; AD044071.
XX
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
PS Claim 22; Page 75-76; 101pp; English.
XX
CC The present sequence represents a fusion protein, comprising E7 and E6
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E7E6Pentm, and comprises an E7 amino terminus
CC (where residues 24, 26 and 91 have been replaced with glycine) and an E6
CC carboxy terminus (where residues 63 and 106 have been replaced with an
CC glycine). E7E6Pentm is representative of fusion proteins of the
CC invention. The specification describes human papillomavirus E6 and E7

CC polypeptides, where the E7 polypeptide has mutations at any one or more
CC of the amino acids corresponding to amino acids 24, 26 or 31 of the
CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has
CC mutations at any one or more of the amino acids corresponding to amino
CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of
CC the invention are useful for treating or preventing human papillomavirus
CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins
CC and nucleic acids encoding the fusion proteins are useful for generating
CC immune responses against HPV. They are also useful for treating lower
CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of
CC the reproductive system, including penile and vulvar cancer.

XX Sequence 248 AA:

Query Match 99.4%; Score 514; DB 8; Length 248;
Best Local Similarity 96.9%; Pred. No. 3.9e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEVMDLPQETTDLYXXKOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
ID |||||||
XX 1 MHGDPPTLHEVMDLPQETTDLYXXKOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
Db |||||||
QY 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98
ID |||||||
Db 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98

RESULT 2
AED13079 standard; protein; 98 AA.

XX AED13079;
AC
XX
XX 15-DEC-2005 (first entry)

DT
XX
XX HPV16 E7 variant protein sequence.

DE
XX
XX mutagen; vaccine; antigen; virucide; antibacterial.

KM
XX
XX Human papillomavirus type 16.

OS
XX
XX FR2868781-A1.

PN
XX
XX 14-OCT-2005.

PD
XX
XX 13-APR-2004; 2004FR-00003848.

PF
XX
XX 13-APR-2004; 2004FR-00003848.

PR
XX
XX 13-APR-2004; 2004FR-00003848.

XX
XX
XX (IMMU-) IMMUTEP.

PA
XX
XX Triebel F;

PI
XX
XX WPI; 2005-678227/70.

DR
XX
XX N-PSDB; AED13077.

XX
XX
XX Therapeutic vaccine, for viral and bacterial conditions, comprises an
PT antigen protein and a viral or bacterial protein, coupled together by
PT stable hydrogen or covalent bonds in biological media.

XX
XX
XX Disclosure; Fig 1; 51pp; French.

XX
XX
XX The invention relates to a novel vaccine composed of an antigen protein

CC and a second protein as an 8-(methyl mercury)-1-cysteine (CmH class II)

CC ligand. The second protein is taken from a group including human

CC Lymphocyte Activation Gene (LhAG)-3. The first protein is a viral or

CC bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures.

CC The viral antigens can be for hepatitis B (HBV), human papillomavirus
CC (HPV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-
CC Barr virus (EBV), cytomegalovirus (CMV), and their combinations. The
CC bacterial antigens can be intracellular bacteria of tuberculosis, leprosy
CC and listeria. A vaccine of the invention has virucide, and antibacterial
CC activity. The present sequence represents the HPV16 variant E7 protein

CC sequence.

XX Sequence 98 AA;

QY 99.2%; Score 513; DB 9; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.6e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEVMDLPQETTDLYXXKOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
ID |||||||
XX 1 MHGDPPTLHEVMDLPQETTDLYXXKOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
Db |||||||
QY 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98
ID |||||||
Db 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98

RESULT 3

AA25378
ID AAY25378 standard; protein; 220 AA.

XX AAY25378;

AC
XX
XX 06-SEP-1999 (first entry)

DT
XX
XX HPV fusion protein D1/3-E7-Mutated(C24G,E26Q)/HPV16.

DE
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7, immunomodulator; tumour;

KW immunological fusion partner; CpG oligonucleotide; immune response;

KW HPV antigen; prevention; treatment.

XX
XX
XX Synthetic.

OS
XX
XX Human papillomavirus.

PN
XX
XX WO933868-A2.

PD
XX
XX 08-JUL-1999.

XX
XX
XX 18-DEC-1998; 98WO-EP008563.

XX
XX
XX 24-DEC-1997; 97GB-00027262.

XX
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

PA
XX
XX Dalemans WLJ, Gerard CMG;

PI
XX
XX WPI; 1999-405485/34.

DR
XX
XX N-PSDB; AAY78794.

XX
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV.

XX
XX
XX Example V, Page 51; 62pp; English.

XX
XX
XX AAY78791-X78801 represent nucleic acid sequences which encode novel

CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from

CC HPV (represented in AAY25375-Y25386). These constructs are optionally

CC linked to an immunological fusion partner and an immunomodulatory CpG

CC oligonucleotide. The products of the invention can be used to induce an

CC immune response in a patient to an HPV antigen. They can also be used for

CC preventing or treating HPV induced tumours

XX
XX
XX Sequence 220 AA:

Query Match 99.2%; Score 513; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 4.6e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEVMDLPQETTDLYXXKOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
ID |||||||
XX 1 MHGDPPTLHEVMDLPQETTDLYXXKOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 60
Db |||||||
QY 114 MHGDPPTLHEVMDLPQETTDLYXXKOLNDSSEDEIDGPAGQAEPRRAHYNIVTFCK 173
ID |||||||
Db 61 CDSTLRFCVOSTHVDIRTLIEDLIMGTLGIYXPCSQKP 98

Db 174 CDSTLRUCVOSTHYDRTLEDLMTGLGIVCPICSQKP 211

|||||

RESULT 4
AA02634
ID AA02634 standard; protein; 220 AA.
XX
AC AA02634;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot.D1/3-E7-mut(C24G,E26Q)/HPV16 protein.
XX
DE Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KW tumour; lesion; benign; malignant; virus; infection.
XX
OS Human papillomavirus.
OS Chimeric.
OS Haemophilus influenzae.
OS Chimeric.
XX
PN MO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
DR WPI: 1999-190587/16.
DR N-PSDB; AAX29783.
XX
PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
PS Disclosure; Fig 8; 95pp; English.
XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 220 AA;

Query Match 99.2%; Score 513; DB 2; Length 220;
Best Local Similarity 96.9%; Pred. No. 4.6e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPPRAHYNIVTFCK 60
Db 114 MHGDPPTLHEHMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPPRAHYNIVTFCK 173

QY 61 CDSTLRUCVOSTHYDRTLEDLMTGLGIVCPICSQKP 98
Db 174 CDSTLRUCVOSTHYDRTLEDLMTGLGIVCPICSQKP 211

RESULT 5
AED52640
ID AED52640 standard; protein; 220 AA.
XX
AC AED52640;
XX

DT 29-DEC-2005 (first entry)
XX
DE Fusion protein D1/3-E7-His(HPV16), C137G/E139Q.
XX
KW Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection;
KW virucide; uterine cervix tumor; E7; mucin; D protein.
XX
OS Haemophilus influenzae; strain 772.
OS Human papillomavirus type 16.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Misc-difference 137
FT /note= "Wild-type Cys substituted by Gly"
FT Misc-difference 139
FT /note= "Wild-type Glu substituted by Gln"
XX
PN IN9801903-14.
XX
PD 04-MAR-2005.
XX
PF 24-AUG-1998; 98IN-CH001903.
XX
PR 22-AUG-1997; 97EP-00179535.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Tyrrell AMR;
XX
DR WPI: 2005-557646/57.
DR N-PSDB; AED52639.
XX
PT Vaccine.
XX
PS Example 8; Fig 8; 96pp; English.
XX
CC The invention relates to human Papilloma virus (HPV) fusion proteins,
CC linked to an immunological fusion partner that provides T helper epitopes
CC to the HPV antigen. Vaccine formulations comprising the fusion proteins
CC are useful in the treatment or prophylaxis of HPV induced lesions
CC (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7
CC proteins (singly, as an E6-E7 fusion or mutated) were fused to either
CC Haemophilus influenzae D protein (20-127), the C-terminus of
CC Streptococcus pneumoniae LytA protein (cLYtA) or chloroform. The present
CC sequence represents a mutated HPV-H. influenzae D protein, fusion protein
CC of the invention.
XX
SQ Sequence 220 AA;

Query Match 99.2%; Score 513; DB 9; Length 220;
Best Local Similarity 96.9%; Pred. No. 4.6e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDPPTLHEHMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPPRAHYNIVTFCK 60
Db 114 MHGDPPTLHEHMDLQEPETDLYXXQLNDSSEDEIDGPAQAEPPRAHYNIVTFCK 173

QY 61 CDSTLRUCVOSTHYDRTLEDLMTGLGIVCPICSQKP 98
Db 174 CDSTLRUCVOSTHYDRTLEDLMTGLGIVCPICSQKP 211

RESULT 6
ADO44068
ID ADO44068 standard; protein; 248 AA.
XX
AC ADO44068;
XX
DT 15-JUN-2004 (first entry)
XX
DE Amino acid sequence of a fusion protein designated B7E6frem.
XX

KM E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;
KM cervical cancer; immune response; lower gastrointestinal tract cancer;
KM anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
XX
OS Human papillomavirus type 16.
OS Synthetic.
XX
PN WO2004030636-A2.
XX
PD 15-APR-2004.
XX
PF 02-OCT-2003; 2003WO-US031726.
XX
PR 03-OCT-2002; 2002US-0415929P.
XX
PA (AMHP) WYETH HOLDINGS CORP.
XX
PI Smith L, Caesetti MC;
XX
XX WPI: 2004-316328/29.
DR N-PSDB; ADA04069.
XX
PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,
PT useful for treating or preventing human papillomavirus (HPV)-associated
PT cancers, e.g. cervical cancer.
XX
PS Claim 22: Page 73-74; 101pp; English.
XX
XX The present sequence represents a fusion protein, comprising E7 and E6
CC polypeptides from human papillomavirus type 16 (HPV16). The fusion
CC protein is designated E7E6tetw, and comprises an E7 amino terminus (where
CC residues 24 and 26 have been replaced with glycine) and an E6 carboxy
CC terminus (where residues 63 and 106 have been replaced with glycine).
CC E7E6tetw is representative of fusion proteins of the invention. The
CC specification describes human papillomavirus E6 and E7 polypeptides,
CC where the E7 polypeptide has mutations at any one or more of the amino
CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in
CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any
CC one or more of the amino acids corresponding to amino acids 63 or 106 of
CC the sequence given in ADO44072. The polypeptides of the invention are
CC useful for treating or preventing human papillomavirus (HPV)-associated
CC cancers, such as cervical cancer. The fusion proteins and nucleic acids
CC encoding the fusion proteins are useful for generating immune responses
CC against HPV. They are also useful for treating lower gastrointestinal
CC tract cancers, e.g. anal cancer, and other cancers of the reproductive
CC system, including penile and vulvar cancer.
XX
SQ Sequence 248 AA:
Query Match 99.2%; Score 513; DB 8; Length 248;
Best Local Similarity 96.9%; Pred. No. 5.3e-57; Mismatches 3; Indels 0; Gaps 0;
Matches 95; Conservative 0;
Qy 1 MHGPTPLHEHYMDLOPETTDLYXXQLNDSSEEDIDDPAGQAEPRRAHYNIIVTFCK 60
Db 1 MHGPTPLHEHYMDLOPETTDLYGYQLNDSSEEDIDDPAGQAEPRRAHYNIIVTFCK 60
Qy 61 CDSTLRCLCVOSTHVDIRTLIEDLMLGTIGIYCPICQKP 98
Db 61 CDSTLRCLCVOSTHVDIRTLIEDLMLGTIGIYCPICQKP 98
RESULT 7
ADA27366
ID ADA27366 standard; protein; 805 AA.
XX
AC ADA27366;
XX
DT 20-NOV-2003 (first entry)
XX
DE HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.
XX
KM cell line; American Type Culture Collection PTA-4047; ATCC-4047;

KM baculoviruses; viral recombinant protein; virus-like particle; vaccine;
KM diagnostic reagent; human papillomavirus type 16; HPV-16; L2/E7/E2;
KM fusion protein.
XX
OS Synthetic.
OS Human papillomavirus type 16.
XX
PN WO2003068804-A2.
XX
PD 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-US004516.
XX
PF 14-FEB-2002; 2002US-0356113P.
PR 14-FEB-2002; 2002US-0356118P.
PR 14-FEB-2002; 2002US-0356119P.
PR 14-FEB-2002; 2002US-0356123P.
PR 14-FEB-2002; 2002US-0356126P.
PR 14-FEB-2002; 2002US-0356133P.
PR 14-FEB-2002; 2002US-0356135P.
PR 14-FEB-2002; 2002US-0356150P.
PR 14-FEB-2002; 2002US-0356151P.
PR 14-FEB-2002; 2002US-0356152P.
PR 14-FEB-2002; 2002US-0356152P.
PR 14-FEB-2002; 2002US-0356154P.
PR 14-FEB-2002; 2002US-0356156P.
PR 14-FEB-2002; 2002US-0356157P.
PR 14-FEB-2002; 2002US-0356161P.
PR 14-FEB-2002; 2002US-0356162P.
XX
XX (NOVA-) NOVAVAX INC.
XX
PA Robinson RA;
XX
PI WPI: 2003-646475/61.
XX
DR N-PSDB; ADA27374.
XX
XX New insect cell line designated ATCC PTA-4047, useful for replicating
PT baculoviruses to produce large amounts of recombinant proteins of
PT medical, pharmaceutical and veterinary importance.
XX
XX Disclosure; Page 59-60; 63pp; English.
XX
PS The present invention describes a cell line comprising a cell that is a
CC clone, derivative, mutant and/or transfectant of a cell line designated
CC American Type Culture Collection (ATCC) PTA-4047. The cell upon culture
CC grows continuously and retains the identifying characteristics of the
CC cell line designated ATCC-4047. Also described is a process of making a
CC cell line. The insect cell line is useful in replicating baculoviruses,
CC as a host substrate for baculovirus plaque assays, as a source of insect
CC proteins, acts as a depot for cell transfection to produce recombinant
CC baculoviruses, and in expressing viral recombinant proteins.
CC Extracellular and intracellular viral recombinant proteins and virus-like
CC particles expressed from the cell line are useful as pharmaceutical
CC compositions, vaccines or diagnostic reagents. The present sequence
CC represents a human papillomavirus type 16 (HPV-16) L2/E7/E2 fusion
CC protein, which is used in the exemplification of the present invention.
XX
SQ Sequence 805 AA:
Query Match 99.2%; Score 513; DB 6; Length 805;
Best Local Similarity 96.9%; Pred. No. 2.4e-56; Mismatches 3; Indels 0; Gaps 0;
Matches 95; Conservative 0;
Qy 1 MHGPTPLHEHYMDLOPETTDLYXXQLNDSSEEDIDDPAGQAEPRRAHYNIIVTFCK 60
Db 471 MHGPTPLHEHYMDLOPETTDLYGYQLNDSSEEDIDDPAGQAEPRRAHYNIIVTFCK 530
Qy 61 CDSTLRCLCVOSTHVDIRTLIEDLMLGTIGIYCPICQKP 98
Db 531 CDSTLRCLCVOSTHVDIRTLIEDLMLGTIGIYCPICQKP 568
RESULT 8

ADA92544
ID ADA92544 standard; protein; 805 AA.
XX
AC ADA92544;
XX
DT 20-NOV-2003 (first entry)
XX
DE HPV-16 L2/E7/E2 fusion amino acid sequence SEQ ID NO:9.
XX
XX codon optimised; viral capsid protein; virus-like particle; VLP;
KM antigenic; human papillomavirus infection; virucide; vaccine;
KW gene therapy; human papillomavirus type 16; dysplasia; infection; HPV-16;
XX fusion protein.
XX
OS Synthetic.
XX Human papillomavirus type 16.
XX
PN WO2003068933-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US004480.
XX
PR 14-FEB-2002; 2002US-0356113P.
PR 14-FEB-2002; 2002US-0356118P.
PR 14-FEB-2002; 2002US-0356119P.
PR 14-FEB-2002; 2002US-0356123P.
PR 14-FEB-2002; 2002US-0356126P.
PR 14-FEB-2002; 2002US-0356133P.
PR 14-FEB-2002; 2002US-0356135P.
PR 14-FEB-2002; 2002US-0356150P.
PR 14-FEB-2002; 2002US-0356151P.
PR 14-FEB-2002; 2002US-0356152P.
PR 14-FEB-2002; 2002US-0356154P.
PR 14-FEB-2002; 2002US-0356156P.
PR 14-FEB-2002; 2002US-0356157P.
PR 14-FEB-2002; 2002US-0356161P.
PR 14-FEB-2002; 2002US-0356162P.
XX
PA (NOVA-) NOVAVAX INC.
XX
PI Robinson RA;
XX
XX WPI: 2003-689664/65.
DR N-PSDB; ADA92552.
DR
XX
XX New codon optimized polynucleotide encoding a viral capsid protein that
PT self assembles into a virus-like particle, useful for diagnosing,
PT preventing or treating human papillomavirus infections or associated
PT disorders.
XX
XX
PS Disclosure; Page 119-120; 123pp; English.
XX
XX The present invention describes a codon optimised polynucleotide encoding
CC a viral capsid protein that self assembles into a virus-like particle
CC (VLP) that exhibits conformational antigenic epitopes capable of raising
CC neutralising antibodies, where the VLP is expressed from a host cell
CC extracellularly. Also described: (1) a vector comprising the above codon
CC optimised polynucleotide operably linked to a eukaryotic or prokaryotic
CC regulatory control element, capable of replication in prokaryotic and/or
CC eukaryotic host; (2) a host cell comprising the vector; (3) a
CC pharmaceutical or vaccine composition for treating, ameliorating or
CC preventing a papillomavirus related disease or disorder, comprising a
CC multiplicity of VLPs that exhibit conformational antigenic epitopes, and
CC a carrier, diluent or adjuvant; (4) a diagnostic kit for detecting a
CC papillomavirus infection, comprising a multiplicity of VLPs that exhibit
CC conformational antigenic epitopes, and a detection agent comprising a
CC detectable label; (5) a method for preparing the above codon optimised
CC polynucleotide, comprising replacing codons that are underutilised in
CC insect cells with codons that are utilised at high levels in insect
CC cells, to create an initially-modified nucleotide sequence, and modifying
CC the initially-modified nucleotide sequence by choosing a preferred codon
CC for the initially-modified sequence, where the ratio of GC nucleotide

CC pairs to AT nucleotide pairs in the further-modified nucleotide sequence
CC trends towards about 1:1, where the number of palindromic and stem-loop
CC DNA structures in the further-modified nucleotide sequence is minimised,
CC and where the number of transcription and post-transcription repressor
CC elements are minimised; and (6) methods for treating, ameliorating or
CC preventing a papillomavirus related disease or disorder, or for
CC protecting an individual against a papillomavirus infection, comprising
CC administering to an individual an amount of the composition or vaccine
CC cited above. The VLP has virucide activity and can be used in vaccines
CC and in gene therapy. The composition and methods of the present invention
CC are useful in diagnosing, preventing or treating human papillomavirus
CC infections or associated disorders, such as dysplasia. The present
CC sequence represents an HPV-16 codon optimised L2/E7/E2 fusion amino acid
CC sequence from the present invention.
XX
XX
SQ Sequence 805 AA;
XX
XX
Query Match 99.2%; Score 513; DB 7; Length 805;
Best Local Similarity 96.9%; Pred. No. 2.4e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHEVMDLPETTDLYXXYXQLNDSSEDEIDGPAQAEPPRAHNYITVFCCK 60
DB 471 MHGDTPTLHEVMDLPETTDLYXGEQLNDSSEDEIDGPAQAEPPRAHNYITVFCCK 530
QY 61 CDSTRLCVOSTHVDIRLTEDLNGTIGIYXPCSQKP 98
DB 531 CDSTRLCVOSTHVDIRLTEDLNGTIGIYVPCSQKP 568
RESULT 9
ADA14293
ID ADA14293 standard; protein; 805 AA.
XX
XX ADA14293;
AC
XX
DT 06-NOV-2003 (first entry)
XX
XX
XX HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.
DE
XX
KM purification; recombinant extracellular virus-like particle;
KM recombinant intracellular virus-like particle; virus-like particle; VLP;
KM virucide; vaccine; gene therapy; human papillomavirus; HPV; infection;
KM dysplasia; HPV-16; fusion protein.
XX
XX
OS Synthetic.
OS Human papillomavirus type 16.
XX
XX
XX WO2003068933-A1.
XX
XX
XX 21-AUG-2003.
PD
XX
XX 14-FEB-2003; 2003WO-US004474.
PF
XX
XX 14-FEB-2002; 2002US-0356113P.
PR 14-FEB-2002; 2002US-0356118P.
PR 14-FEB-2002; 2002US-0356119P.
PR 14-FEB-2002; 2002US-0356123P.
PR 14-FEB-2002; 2002US-0356126P.
PR 14-FEB-2002; 2002US-0356133P.
PR 14-FEB-2002; 2002US-0356135P.
PR 14-FEB-2002; 2002US-0356150P.
PR 14-FEB-2002; 2002US-0356151P.
PR 14-FEB-2002; 2002US-0356152P.
PR 14-FEB-2002; 2002US-0356154P.
PR 14-FEB-2002; 2002US-0356156P.
PR 14-FEB-2002; 2002US-0356157P.
PR 14-FEB-2002; 2002US-0356161P.
PR 14-FEB-2002; 2002US-0356162P.
XX
XX
XX (NOVA-) NOVAVAX INC.
PA
XX Robinson RA, Thompson MW;
PI

XX WP1: 2003-679645/64.
DR N-PSDB; ADA13301.
XX
PT Purifying a recombinant human papillomavirus (HPV) L1, useful for
PT diagnosing, preventing or treating HPV infections, comprises clarifying,
PT concentrating and dialyzing cells containing HPV particles.
XX
PS Disclosure; Page 103-104; 11pp; English.
XX
XX The present invention describes a method for purifying a recombinant
CC extracellular or intracellular virus-like particle (VLP). The method
CC comprises harvesting a cell suspension comprising cells containing a
CC plurality of VLPS to produce a harvested supernatant, optionally
CC disrupting the harvested cells to produce cell lysates containing the
CC VLP, clarifying the harvested supernatant, concentrating the clarified
CC supernatant, dialyzing the concentrated supernatant, and recovering
CC the purified recombinant VLP. Also described: (1) a cell line designated
CC as Sf-9S deposited as American Type Culture Collection (ATCC) PTA-4047;
CC (2) producing the cell line described above; (3) host cells that express
CC one or more recombinant gene products with an enhanced yield; (4)
CC producing a foreign protein in an insect cell; (5) nucleic acid sequences
CC that correspond to and code for human papillomavirus (HPV) polypeptides;
CC and (6) pharmaceutical compositions comprising an amount of the
CC recombinant viral gene products, VLPS, agonists, antagonists, or the
CC active fragment of a viral gene product. The VLPS have virulence activity,
CC and can be used in vaccines and in gene therapy. The method is useful in
CC isolating and purifying expressed viral gene products, including VLPS, in
CC vitro. The gene products or particles may be used in detecting,
CC preventing or treating HPV infections and associated symptoms, like
CC dysplasia. The present sequence represents an HPV-16 L2/E7/E2 fusion
CC protein, which is given in the exemplification of the present invention.
XX
SQ Sequence 805 AA:

Query Match 99.2%; Score 513; DB 7; Length 805;
Best Local Similarity 96.9%; Pred. No. 2.4e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEMYMDLQPEPTTDLXXYXQNDSSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
DB 471 MHGDTPTLHEMYMDLQPEPTTDLXXYXQNDSSSEEDIDGPAGQAEPRRAHYNIVTFCK 530
QY 61 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 98
DB 531 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 568

RESULT 10
AAB38618
ID AAB38618 standard; protein; 805 AA.
XX
AC AAB38618;
XX
DT 04-DEC-2003 (first entry)
XX
DE HPV-16 L2/E7/E2 fusion protein.
XX
XX Vaccine; humoral immunity; cell-mediated immunity; gene therapy; HPV,
KW virucide; papillomavirus infection; Human papillomavirus; fusion protein.
XX
OS Human papillomavirus.
OS Synthetic.
XX
PN WO2003068163-A2.
XX
PD 21-AUG-2003.
XX
PF 14-FEB-2003; 2003WO-US0044473.
XX
PR 14-FEB-2002; 2002US-0356113P.
PR 14-FEB-2002; 2002US-0356118P.
PR 14-FEB-2002; 2002US-0356119P.

PR 14-FEB-2002; 2002US-0356123P.
PR 14-FEB-2002; 2002US-0356126P.
PR 14-FEB-2002; 2002US-0356133P.
PR 14-FEB-2002; 2002US-0356135P.
PR 14-FEB-2002; 2002US-0356150P.
PR 14-FEB-2002; 2002US-0356151P.
PR 14-FEB-2002; 2002US-0356152P.
PR 14-FEB-2002; 2002US-0356154P.
PR 14-FEB-2002; 2002US-0356156P.
PR 14-FEB-2002; 2002US-0356157P.
PR 14-FEB-2002; 2002US-0356161P.
PR 14-FEB-2002; 2002US-0356162P.

PA (NOVA-) NOVAVAX INC.
XX
P1 Robinson RA, Cloce V;
XX
XX WP1: 2003-689598/65.
DR N-PSDB; AAD58574.
XX

PT New chimeric virus-like particles comprising a recombinant viral capsid
PT protein encapsulating a recombinant viral protein, useful for inducing
PT humoral and/or cell-mediated immunity against papillomavirus infection.
XX
PS Disclosure; Page 122-123; 126pp; English.

XX The present invention relates to chimeric virus-like particle comprising
CC a recombinant viral capsid protein that encapsulates a recombinant viral
CC protein during self assembly into a chimeric virus-like particle and
CC exhibiting conformational antigenic epitopes capable of eliciting
CC neutralising antibodies. The vaccine comprising the chimeric virus-like
CC particles are useful for inducing immunity (humoral and/or cell-mediated
CC immunity) against papillomavirus infection. The invention is also useful
CC in gene therapy. The present sequence is HPV (human papillomavirus)-16
CC L2/E7/E2 fusion protein
XX
SQ Sequence 805 AA:

Query Match 99.2%; Score 513; DB 7; Length 805;
Best Local Similarity 96.9%; Pred. No. 2.4e-56;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEMYMDLQPEPTTDLXXYXQNDSSSEEDIDGPAGQAEPRRAHYNIVTFCK 60
DB 471 MHGDTPTLHEMYMDLQPEPTTDLXXYXQNDSSSEEDIDGPAGQAEPRRAHYNIVTFCK 530
QY 61 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 98
DB 531 CDSTLRLCVOSTHVDIRTELDLMGTGIGYXPICSQKP 568

RESULT 11
AAR22767
ID AAR22767 standard; peptide; 98 AA.
XX
AC AAR22767;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1992 (first entry)
XX
DE HPV E7 peptide.
XX
KW Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9205248-A.
XX
PD 02-APR-1992.
XX
PF 26-SEP-1991; 91WO-US007081.
XX

PR 26-SEP-1990; 90US-00588384.
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL,
XX WPI; 1992-132119/16.
XX
XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and
XX recombinant cells encoding them, useful in treatment and prophylaxis of
XX cervical warts or cancer resulting from HPV infection.
XX
XX Disclosure; Fig 7; 81pp; English.
XX
XX The peptide is the sequence of the human papillomavirus HPV 16 E7
XX nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)
XX of HPV 16 E7 were synthesized by standard Merrifield synthesis. Examples
XX of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these
XX peptides, antibodies against the peptides, or recombinant cells contg.
XX the gene encoding the immunogenic peptides may be utilized in methods for
XX inhibiting and treating HPV infection and tumour initiation and
XX progression e.g. in the prevention or rebaration of cervical warts and
XX cervical carcinoma resulting from HPV infection. See also AAR22766.
XX (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 98 AA:
SQ

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPTLHEWMLDQPEPTTDLXXYXQUNDSSSEEDSIDGPAQAEPDRAHNYITFCCK 60
DB 1 MGGDTPTLHEWMLDQPEPTTDLXXYXQUNDSSSEEDSIDGPAQAEPDRAHNYITFCCK 60
QY 61 CDSTRLCVOSTHVDIRTELDLMTGLGIYVPCISQKP 98
DB 61 CDSTRLCVOSTHVDIRTELDLMTGLGIYVPCISQKP 98

RESULT 12
AAR42361
ID AAR42361 standard; protein; 98 AA.
XX
XX AAR42361;
AC
XX 25-MAR-2003 (revised)
DT 21-MAY-1994 (first entry)
XX
XX Human papillomavirus 16 E7 protein and fragments.
DE
XX Tumours; cows; horses; donkeys; regression; udder warts; HPV16.
KM
XX Synthetic.
OS
XX W09320844-A1.
PN 28-OCT-1993.
XX
XX 01-APR-1993; 93WO-GB000679.
PF
XX 08-APR-1992; 92GB-00007701.
PR
XX (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
PA
XX Camp MS;
PI
XX WPI; 1993-351368/44.
DR
XX Use of papilloma-virus E7 protein or fragments for the therapy of
PT papilloma-virus disease - for the regression of tumours e.g. removal of
PT warts from udders or mouth of milking cows or for treatment of horses or

PT donkeys.

XX Disclosure; Fig 2; 31pp; English.

XX The sequence is that of the human papillomavirus type 16 E7 protein. The
XX protein sequence was aligned with that of bovine papillomavirus type 4.
XX See also AAR42360. (Updated on 25-MAR-2003 to correct PN field.)
XX

SQ Sequence 98 AA;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGGDTPTLHEWMLDQPEPTTDLXXYXQUNDSSSEEDSIDGPAQAEPDRAHNYITFCCK 60
DB 1 MGGDTPTLHEWMLDQPEPTTDLXXYXQUNDSSSEEDSIDGPAQAEPDRAHNYITFCCK 60
QY 61 CDSTRLCVOSTHVDIRTELDLMTGLGIYVPCISQKP 98
DB 61 CDSTRLCVOSTHVDIRTELDLMTGLGIYVPCISQKP 98

RESULT 13

AAW4686
ID AAW4686 standard; protein; 98 AA.

XX AAW4686;

AC
XX 25-MAR-2003 (revised)
DT 15-JUN-1998 (first entry)

DE Amino acid sequence of the HPV-16 E7 oncoprotein.

XX E7 oncoprotein; proliferative state; HPV; kinase activity;
XX cyclin/cyclin-dependent kinase; p21CIP1; interaction; inactivation;
XX cyclin/cyclin-dependent kinase inhibitor.

OS Human papillomavirus.

XX US5736318-A.

XX 07-APR-1998.

XX 17-MAR-1995; 95US-00406248.

XX 17-MAR-1995; 95US-00406248.

XX (HARD) UNIV HARVARD.

XX (HARD) HARVARD COLLEGE.

XX Muenger K, Jones DL;

XX WPI; 1998-239202/21.

XX N-PSDB; AAV16717.

XX Evaluation of proliferative state of cells transformed with human
PT papilloma virus - by determining cyclin-dependent kinase activity induced
PT by E7 onco-protein.

XX Disclosure; Col 19-20; 14pp; English.

XX The present sequence represents Human papillomavirus (HPV), strain 16, E7
XX oncoprotein. The proliferative state of a cell transformed with HPV can
XX be evaluated in the following manner. Cyclin/cyclin-dependent kinase
XX complexes containing protein p21CIP1 (AAW4687-88) are isolated from the
XX transformed cell, and the HPV E7 oncoprotein added to the isolated
XX protein. Cyclin/cyclin-dependent kinase complexes are isolated from an
XX untransformed cell that is substantially homologous with the transformed
XX cell, and the HPV E7 oncoprotein added. The kinase activities of the 2
XX samples are measured, where a proliferating transformed cell has a
XX greater kinase activity than the untransformed cell. The method is used
XX for determining the extent of interaction and/or inactivation between a

CC cyclin/cyclin-dependent kinase inhibitor and the HPV E7 oncoprotein and
CC thus evaluating the proliferative state of a transformed cell. (Updated
CC on 25-MAR-2003 to correct PI field.)

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 2; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 MGGDPTLHEHYMLDLOPETTDLYXXYXQLNDSSEBEDEIDGPAGAEPRRAHNYIVTFCK 60

1 MGGDPTLHEHYMLDLOPETTDLYCYEQLNDSSEBEDEIDGPAGAEPRRAHNYIVTFCK 60

61 CDSTLRLCVQSTHVDIRTLBDMGTGIGYXPICSQKP 98

61 CDSTLRLCVQSTHVDIRTLBDMGTGIGYXPICSQKP 98

Db

AAV58474 standard; protein; 98 AA.

AAV58474;

10-APR-2000 (first entry)

Human papillomavirus (HPV) E7 oncoprotein.

HPV E7 oncoprotein; proteasome activity; degradation; virus component;

virucide; inflammatory disease; anti-inflammatory; anti-HIV;

Human papillomavirus.

MO9966065-A2.

23-DEC-1999.

10-JUN-1999; 99WO-GB001840.

13-JUN-1998; 98GB-00012756.

13-JUN-1998; 98GB-00012757.

13-JUN-1998; 98GB-00012758.

13-JUN-1998; 98GB-00012759.

13-JUN-1998; 98GB-00012760.

(BRID-) BRIDGEHEAD TECHNOLOGIES LTD.

Schmid H, Petit F, Kioetzel P, Jarrouse A, Gautier K, Badaoui S;

Mouzevay S, Nicolas P;

WPI; 2000-106109/09.

Novel assay methods for identifying compounds which modulate and/or

regulate proteasomal activity.

Disclosure; Page 8; 35pp; English.

The invention relates to a novel assay for identifying compounds which

inhibit viral replication and pathogenesis by increasing proteasomal

degradation of viral components or molecules induced by viral infection.

The method comprises reacting a compound with proteasomal protein (20S.

proteasomes separately with or without 19S and 11S complexes), viral gene

product, and protein or peptide substrates; measuring protease activity;

and identifying the compound as an inhibitor if the protease activity of

the assay system is increased. The assays of the invention can be used to

identify compounds which inhibit viral replication and pathogenesis, and

modulate and/or regulate proteasome activity. Compounds which increase

proteasomal degradation of viral components or molecules induced by viral

infection are of value in the treatment of viral disease. Compounds which

modulate proteasomal nuclease activity have use in the treatment of

inflammatory disease, and AIDS in HIV infected patients. The methods may

CC also be used to generate resistance to bacterial or viral damage.

XX Sequences AAV58472-Y58474 represent examples of viral proteins which

CC affect proteasomal function

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 3; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

1 MGGDPTLHEHYMLDLOPETTDLYXXYXQLNDSSEBEDEIDGPAGAEPRRAHNYIVTFCK 60

1 MGGDPTLHEHYMLDLOPETTDLYCYEQLNDSSEBEDEIDGPAGAEPRRAHNYIVTFCK 60

61 CDSTLRLCVQSTHVDIRTLBDMGTGIGYXPICSQKP 98

61 CDSTLRLCVQSTHVDIRTLBDMGTGIGYXPICSQKP 98

Db

AAV57721 standard; protein; 98 AA.

AAV57721;

14-MAR-2000 (first entry)

Human papillomavirus 16 E7 protein SEQ ID NO:4.

Human papillomavirus; HPV; L1 fusion protein; vaccine; cytostatic;

virucide; dermatological; malignant tumour formation;

cervical cancer; cervical intraepithelial neoplasia; genital wart;

condylomata acuminata.

Human papillomavirus.

CA2229955-A1.

20-AUG-1999.

20-FEB-1998; 98CA-02229955.

20-FEB-1998; 98CA-02229955.

(MEDI-) MEDIGENE GMBH.

Burger A, Hallik M,

WPI; 2000-063092/06.

N-PSDB; AAZ48175.

Fusion proteins comprising papillomavirus specific proteins useful for

vaccinating against malignant tumors of the anogenital tract such as

cervical carcinomas.

Example 1; Page 34; 46pp; English.

The present invention describes a fusion protein comprising 2 amino acids

sequences from 2 different papillomavirus specific (PVS) proteins. The

fusion protein may be administered for preventing and treating

papillomavirus infections in humans and animals. Papillomaviruses are

implicated in the pathology of malignant tumour formation in the

anogenital tract (of these tumours, cervical cancer is the most frequent

(500000 cases/year) and in the formation of precursor lesions of cervical

intraepithelial neoplasia (CIN). Papillomaviruses also cause benign

genital warts such as condylomata acuminata. However, the type and

severity of disease caused by the papillomavirus is dependent on the

strain causing the infection. The present sequence represents the human

papillomavirus 16 E7 protein

XX Sequence 98 AA;

Query Match 99.0%; Score 512; DB 3; Length 98;

Best Local Similarity 96.9%; Pred. No. 2.2e-57;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLTLEHWLMDLOPETTDLYXXQLNDSSSEDEIGPAGQAEPDRAHNYINTFFCK 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MHGDTPLTLEHWLMDLOPETTDLYCYEQLNDSSEDEIDGPAGAEPDRAHNYINTFFCK 60

Db 1 MHGDTPTLHEYMLDQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPRAHYNI VTFCK 60

61 CDSTLRICVQSTHVDIRILEDLLMGTLGIYXPICSQKP 98

Db 61 CDSTLRLCVQSTHVDIRLTLEDLLMGTGLGIVCPICSQKP 98

Search completed: June 6, 2006, 12:04:32
Job time : 146.655 secs

Job time : 146.655 secs

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OM protein - protein search, using SW model

Run on: June 6, 2006, 12:11:25 ; Search time 28.7309 Seconds

(without alignments)
298.563 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517
Sequence: 1 MHGPTLHEHYMLDLPETT.....LEDLMTGLGVXPCSQKP 98

Scoring table:

BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H.COMB.pep.*
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6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE.COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backffile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	513	99.2	220	2	US-09-485-885-8
2	512	99.0	98	1	US-08-406-248-6
3	512	99.0	98	2	US-08-075-541D-42
4	512	99.0	98	2	US-09-382-616A-1
5	512	99.0	98	2	US-08-944-368A-4
6	512	99.0	98	2	US-09-820-764-4
7	512	99.0	98	2	US-09-986-118A-4
8	512	99.0	98	2	US-09-728-466-1
9	512	99.0	98	2	US-09-824-017-4
10	512	99.0	98	2	US-09-637-746-3
11	512	99.0	98	2	US-09-501-097A-7
12	512	99.0	98	2	US-09-980-523A-12
13	512	99.0	121	2	US-09-613-303-12
14	512	99.0	121	2	US-10-267-311-12
15	512	99.0	198	2	US-09-613-303-35
16	512	99.0	198	2	US-10-267-311-35
17	512	99.0	220	2	US-09-485-885-1
18	512	99.0	253	2	US-09-485-885-12
19	512	99.0	253	1	US-08-459-818-20
20	512	99.0	253	1	US-08-889-666-20
21	512	99.0	253	1	US-08-465-078-20
22	512	99.0	253	1	US-08-725-776-20
23	512	99.0	253	1	US-08-488-062-20
24	512	99.0	266	1	US-08-117-083-9
25	512	99.0	266	2	US-08-860-165-10
26	512	99.0	266	2	US-09-359-382-10

27	512	99.0	266	2	US-09-367-309A-1	Sequence 1, Appli
28	512	99.0	287	2	US-09-501-097A-25	Sequence 25, Appl
29	512	99.0	295	2	US-09-613-303-33	Sequence 33, Appl
30	512	99.0	295	2	US-10-267-311-33	Sequence 33, Appl
31	512	99.0	324	2	US-09-613-303-25	Sequence 25, Appl
32	512	99.0	324	2	US-10-267-311-25	Sequence 25, Appl
33	512	99.0	371	2	US-09-485-885-6	Sequence 6, Appli
34	512	99.0	390	2	US-09-485-885-14	Sequence 14, Appl
35	512	99.0	493	2	US-09-613-303-19	Sequence 19, Appl
36	512	99.0	493	2	US-10-267-311-19	Sequence 19, Appl
37	512	99.0	639	2	US-09-613-303-17	Sequence 17, Appl
38	512	99.0	639	2	US-10-267-311-17	Sequence 17, Appl
39	512	99.0	641	2	US-09-613-303-51	Sequence 51, Appl
40	512	99.0	641	2	US-10-267-311-51	Sequence 51, Appl
41	512	99.0	647	2	US-09-613-303-53	Sequence 53, Appl
42	512	99.0	647	2	US-10-267-311-53	Sequence 53, Appl
43	507	98.1	98	2	US-09-566-420-19	Sequence 19, Appl
44	507	98.1	98	2	US-10-201-764-19	Sequence 19, Appl
45	503	97.3	98	2	US-09-613-303-8	Sequence 8, Appli

ALIGNMENTS

```
RESULT 1
US-09-485-885-8
; Sequence 8, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Benchelkh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-8

Query Match          99.2% Score 513, DB 2, Length 220,
Best Local Similarity 96.9% Pred. No. 1.8e-59,
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGPTLHEHYMLDLPETTLYXXOINDSEEDIDGAGQAEPRAHNYITPCK 60
DB 114 MHGPTLHEHYMLDLPETTLYGQOLNDSSEEDIDGAGQAEPRAHNYITPCK 173
61 CDSTRLCVGOSTHVDIRTLBDMGTGLGVPCSQKP 98
174 CDSTRLCVGOSTHVDIRTLBDMGTGLGVPCSQKP 211

RESULT 2
US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
```

```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusner
;; STREET: 200 State Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/406,248
;; FILING DATE:
;; CLASSIFICATION: 436
;; ATTORNEY/AGENT INFORMATION:
;; NAME: McDanielis, Patricia A.
;; REGISTRATION NUMBER: 33,194
;; REFERENCE/DOCKET NUMBER: HAZ-011
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-330-1300
;; TELEFAX: 617-330-1311
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-406-248-6

Query Match          99.0%; Score 512; DB 1; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 MHGDPPTLHEYMLDLPETTDLVYXXQLNDSSSEEDSIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDLPETTDLVYCEQUNDSSSEEDSIDGPAGQAEPPRAHYNIVTFCK 60

Cy 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIYCPICSQKP 98

RESULT 3
US-08-075-541D-42
; Sequence 42, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
```

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;; FILING DATE: 12-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: pct/au91/00575
;; FILING DATE: 12-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: NADEL, ALAN S
;; REGISTRATION NUMBER: 27,363
;; REFERENCE/DOCKET NUMBER: 8795-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-567-2020
;; TELEFAX: 215-567-2991
;; INFORMATION FOR SEQ ID NO: 42:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-075-541D-42

Query Match          99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 MHGDPPTLHEYMLDLPETTDLVYXXQLNDSSSEEDSIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDLPETTDLVYCEQUNDSSSEEDSIDGPAGQAEPPRAHYNIVTFCK 60

Cy 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIYCPICSQKP 98

RESULT 4
US-09-382-616A-1
; Sequence 1, Application US/09382616A
; Patent No. 6200746
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Manxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/382,616A
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
; US-09-382-616A-1

Query Match          99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Cy 1 MHGDPPTLHEYMLDLPETTDLVYXXQLNDSSSEEDSIDGPAGQAEPPRAHYNIVTFCK 60
Db 1 MHGDPPTLHEYMLDLPETTDLVYCEQUNDSSSEEDSIDGPAGQAEPPRAHYNIVTFCK 60

Cy 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIYXPICSQKP 98
Db 61 CDSTLRLCVOSTHVDIRLTEDLMLGTLGIYCPICSQKP 98

RESULT 5
US-08-944-368A-4
; Sequence 4, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
```

;; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
;; NUMBER OF INVENTION: Formulations and Methods of Use
;; CORRESPONDENCE ADDRESSES: 28
;; ADDRESS: Marshall, O'Toole, Gerstein, Murray &
;; ADDRESSEE: Borun
;; STREET: 233 South Wacker Drive, 6300 Sears Tower
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/944,368A
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Williams Jr., Joseph A.
;; REGISTRATION NUMBER: 38,659
;; REFERENCE/DOCKET NUMBER: 27013/34028
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; TELEFAX: 312-474-0448
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-944-368A-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXQLNDSSEEDIDGPAQAEPRAHNYITPCK 60
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQLNDSSEEDIDGPAQAEPRAHNYITPCK 60

Qy 61 CDSTRLCVCOSTHVDIRLTEDLMGTGLGVPCISQKP 98
Db 61 CDSTRLCVCOSTHVDIRLTEDLMGTGLGVPCISQKP 98

RESULT 6
US-09-820-764-4
; Sequence 4, Application US/099820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001

;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/026,896
;; FILING DATE: 20-FEB-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sandercock, Collin G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 37067/102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300
;; TELEFAX: (202) 672-5399
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
;; US-09-820-764-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXQLNDSSEEDIDGPAQAEPRAHNYITPCK 60
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQLNDSSEEDIDGPAQAEPRAHNYITPCK 60

Qy 61 CDSTRLCVCOSTHVDIRLTEDLMGTGLGVPCISQKP 98
Db 61 CDSTRLCVCOSTHVDIRLTEDLMGTGLGVPCISQKP 98

RESULT 7
US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Patent No. 6562351
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,118A
; FILING DATE: 07-No. 6562351-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Collin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRTLIEDLLMGTIGIYXPCSKP 98
DB 61 CDSTLRFCVOSTHVDIRTLIEDLLMGTIGIYXPCSKP 98

RESULT 8
US-09-728-466-1

Sequence 1, Application US/09728466
Patent No. 6641994
GENERAL INFORMATION:
APPLICANT: Fisher, Christopher
APPLICANT: He, Manxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 98
TYPE: PRT
ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRTLIEDLLMGTIGIYXPCSKP 98
DB 61 CDSTLRFCVOSTHVDIRTLIEDLLMGTIGIYXPCSKP 98

RESULT 9
US-09-824-017-4
Sequence 4, Application US/09824017
Patent No. 6649167
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
APPLICANT: HALBEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRTLIEDLLMGTIGIYXPCSKP 98
DB 61 CDSTLRFCVOSTHVDIRTLIEDLLMGTIGIYXPCSKP 98

RESULT 10

US-09-637-746-3
Sequence 3, Application US/09637746
Patent No. 6727079
GENERAL INFORMATION:
APPLICANT: Thorgelsson, Snorri S.
APPLICANT: Moltach, Joseph T.
APPLICANT: Zhang, Minghuang
TITLE OF INVENTION: CDNA ENCODING A GENE BCG (BST OVER-EXPRESSED GENE) AND ITS PROTEIN
FILE REFERENCE: 11613.29USW1
CURRENT APPLICATION NUMBER: US/09/637,746
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PCT/US99/04142
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 60/079,567
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 98
TYPE: PRT
ORGANISM: Human papillomavirus
US-09-637-746-3

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
DB 1 MHGDTPLHEYMLDQPTTDLXXYXQUNDSSSEDEIDGPAGAEPPRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRTLIEDLLMGTIGIYXPCSKP 98

Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

RESULT 11
US-09-501-097A-7
; Sequence 7, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Chou Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 98
; TYPE: PRT
; ORGANISM: human papillomavirus
US-09-501-097A-7

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 1 MHGDTPLHEYMLDQPEPTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98
Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

RESULT 12
US-09-980-523A-12

; Sequence 12, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIERES, ESTELLE
; TITLE OF INVENTION: POLYTOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-12

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 8e-60;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 1 MHGDTPLHEYMLDQPEPTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98

RESULT 13
US-09-613-303-12
; Sequence 12, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-12

Query Match 99.0%; Score 512; DB 2; Length 121;
Best Local Similarity 96.9%; Pred. No. 1.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
Db 24 MHGDTPLHEYMLDQPEPTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 83
Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 98
Db 84 CDSTRLCVOSTHVDIRLTEDLMGTGIVCPICSKP 121

RESULT 14
US-10-267-311-12
; Sequence 12, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-12

Query Match 99.0%; Score 512; DB 2; Length 121;
Best Local Similarity 96.9%; Pred. No. 1.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDQPEPTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60

Db 24 MHGDTPTLHEMYMDLQPETTDLYCYEQUNDSEEEDEIDGPAGQAEPPDRAHYNIVTFCK 83

QY 61 CDSTLRLCVOSTHYDITRTLEDLMLGTLGIYKPICSQKP 98

Db 84 CDSTLRLCVOSTHYDITRTLEDLMLGTLGIYKPICSQKP 121

RESULT 15

US-09-613-303-35
; Sequence 35, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-35

Query Match 99.0%; Score 512; DB 2; Length 198;
Best Local Similarity 96.9%; Pred. No. 2.1e-59;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MHGDTPTLHEMYMDLQPETTDLYXXYXQLNDSSEEEDEIDGPAGQAEPPDRAHYNIVTFCK 60

Db 101 MHGDTPTLHEMYMDLQPETTDLYCYEQUNDSEEEDEIDGPAGQAEPPDRAHYNIVTFCK 160

QY 61 CDSTLRLCVOSTHYDITRTLEDLMLGTLGIYKPICSQKP 98

Db 161 CDSTLRLCVOSTHYDITRTLEDLMLGTLGIYKPICSQKP 198

Search completed: June 6, 2006, 12:13:13
Job time : 29.7309 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:10 ; Search time 106.659 Seconds

(without alignments)
425.611 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517
Sequence: 1 MHGDPPTLHEYMLDLPETT.....LEDLLMGTLGIYVPCISQKP 98

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US07_PUBCOMB pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10_PUBCOMB pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	514	99.4	248	5	US-10-530-253-11 Sequence 11, Appl
2	513	99.2	220	4	US-10-000-903-8 Sequence 8, Appl
3	513	99.2	220	5	US-10-899-771-8 Sequence 8, Appl
4	513	99.2	248	5	US-10-530-253-9 Sequence 9, Appl
5	513	99.2	805	4	US-10-367-095-9 Sequence 9, Appl
6	513	99.2	805	4	US-10-368-046-9 Sequence 9, Appl
7	513	99.2	805	4	US-10-367-367-9 Sequence 9, Appl
8	513	99.2	805	5	US-10-918-337-9 Sequence 9, Appl
9	512	99.0	98	3	US-09-728-466-1 Sequence 1, Appl
10	512	99.0	98	3	US-09-820-765-4 Sequence 4, Appl
11	512	99.0	98	3	US-09-824-017-4 Sequence 4, Appl
12	512	99.0	98	3	US-09-986-118A-4 Sequence 4, Appl
13	512	99.0	98	4	US-10-177-390-8 Sequence 8, Appl
14	512	99.0	98	4	US-10-654-129-4 Sequence 4, Appl
15	512	99.0	98	4	US-10-772-988-3 Sequence 3, Appl
16	512	99.0	98	4	US-10-479-541-5 Sequence 5, Appl
17	512	99.0	98	5	US-10-042-526A-4 Sequence 4, Appl
18	512	99.0	98	5	US-10-657-399-1 Sequence 1, Appl
19	512	99.0	98	5	US-10-858-384-12 Sequence 12, Appl
20	512	99.0	98	5	US-10-343-448-5 Sequence 5, Appl
21	512	99.0	98	5	US-10-367-057-17 Sequence 17, Appl
22	512	99.0	98	5	US-10-530-253-14 Sequence 14, Appl
23	512	99.0	98	6	US-11-077-939-5 Sequence 5, Appl
24	512	99.0	98	6	US-11-179-478-4 Sequence 4, Appl
25	512	99.0	121	4	US-10-267-311-12 Sequence 12, Appl
26	512	99.0	121	5	US-10-679-956-12 Sequence 12, Appl
27	512	99.0	198	4	US-10-267-311-35 Sequence 35, Appl

28	512	99.0	198	5	US-10-679-956-35 Sequence 35, Appl
29	512	99.0	220	4	US-10-000-903-1 Sequence 1, Appl
30	512	99.0	220	5	US-10-899-771-1 Sequence 1, Appl
31	512	99.0	239	4	US-10-000-903-12 Sequence 12, Appl
32	512	99.0	239	5	US-10-899-771-12 Sequence 12, Appl
33	512	99.0	248	5	US-10-530-253-7 Sequence 7, Appl
34	512	99.0	256	6	US-11-192-923A-2 Sequence 2, Appl
35	512	99.0	266	3	US-09-367-309A-1 Sequence 1, Appl
36	512	99.0	295	4	US-10-267-311-33 Sequence 33, Appl
37	512	99.0	295	5	US-10-679-956-33 Sequence 25, Appl
38	512	99.0	324	4	US-10-267-311-25 Sequence 25, Appl
39	512	99.0	324	5	US-10-679-956-25 Sequence 25, Appl
40	512	99.0	334	4	US-10-472-724-10 Sequence 10, Appl
41	512	99.0	371	4	US-10-000-903-6 Sequence 6, Appl
42	512	99.0	371	5	US-10-899-771-6 Sequence 6, Appl
43	512	99.0	390	4	US-10-000-903-14 Sequence 14, Appl
44	512	99.0	390	5	US-10-899-771-14 Sequence 14, Appl
45	512	99.0	421	4	US-10-296-770-7 Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-10-530-253-11
; Sequence 11, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
; APPLICANT: Cassetti, Maria C.
; APPLICANT: Smith, Larry
; APPLICANT: Jeffrey K. Pullen
; APPLICANT: Susan F. McElhinney
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
; FILE REFERENCE: 00630/100M137-US2
; CURRENT APPLICATION NUMBER: US/10/530.253
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US2003/031726
; PRIOR FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: US 60/415,929
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-11
Query Match      99.4%; Score 514; DB 5; Length 248;
Best Local Similarity 96.9%; Pred. No. 3.3e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY      1 MHGDPPTLHEYMLDLPETTLDYXXYXOLDSESEDEIDGPAQAEPPRAHYNYTFCK 60
      |||
DB      1 MHGDPPTLHEYMLDLPETTLDYXXYXOLDSESEDEIDGPAQAEPPRAHYNYTFCK 60
      |||
DB      61 CDSTLRICVGVSTHVDIRLTEDLLMGTLGIYVPCISQKP 98
      |||
DB      61 CDSTLRICVGVSTHVDIRLTEDLLMGTLGIYVPCISQKP 98
      |||
RESULT 2
US-10-000-903-8
; Sequence 8, Application US/10000903
; Publication No. US2002018221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Chislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
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CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-8

Query Match 99.2%; Score 513; DB 4; Length 220;
Best Local Similarity 96.9%; Pred. No. 3,8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEMYMLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60
Db 114 MHGDPPTLHEMYMLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 173

Qy 61 CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVXPICQKP 98
Db 174 CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVCPIQSKP 211

RESULT 3
US-10-899-771-8
Sequence 8, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
PRIOR FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 220
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
OTHER INFORMATION: Influenzae B and mutated E7 from Human papilloma
OTHER INFORMATION: virus type 16)
US-10-899-771-8

Query Match

Best Local Similarity 99.2%; Score 513; DB 5; Length 220;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEMYMLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60
Db 114 MHGDPPTLHEMYMLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 173

Qy 61 CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVXPICQKP 98
Db 174 CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVCPIQSKP 211

RESULT 4
US-10-530-253-9
Sequence 9, Application US/10530253

Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Casaretti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/445,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentn version 3.1
SEQ ID NO 9
LENGTH: 248
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-10-530-253-9

Query Match 99.2%; Score 513; DB 5; Length 248;
Best Local Similarity 96.9%; Pred. No. 4,4e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEMYMLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60
Db 1 MHGDPPTLHEMYMLDLPETTDLYXXYQUNDSEEDIEDGPAGQAEPPRAHNYIVTFCK 60

Qy 61 CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVXPICQKP 98
Db 61 CDSTLRFCVQSTHVDIRTLIEDLMGTIGIVCPIQSKP 98

RESULT 5
US-10-367-095-9
Sequence 9, Application US/10367095
Publication No. US20030228696A1
GENERAL INFORMATION:
APPLICANT: Robin A. Robinson
TITLE OF INVENTION: No. US20030228696A1 Insect Cell line
FILE REFERENCE: 44149-1US1
CURRENT APPLICATION NUMBER: US/10/367,095
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,123
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,113
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,154
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,135
PRIOR FILING DATE: 2002-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
US-10-367-095-9

Query Match 99.2%; Score 513; DB 4; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEWMLDQPEPTTDLXXXQUNDSEEDDEIDGPAQAEPRAHNYITVFCCK 60
Db 471 MGGDPTLHEWMLDQPEPTTDLGYEQUNDSEEDDEIDGPAQAEPRAHNYITVFCCK 530

Qy 61 CDSTRLCVQSTHVDIRLTEDLMGTGIVXPCISQKP 98
Db 531 CDSTRLCVQSTHVDIRLTEDLMGTGIVXPCISQKP 568

RESULT 6
US-10-368-046-9

Sequence 9, Application US/10368046
Publication No. US20040063188A1

GENERAL INFORMATION:

APPLICANT: Robin A. Robinson

APPLICANT: Vitecoria Cioce

TITLE OF INVENTION: Method for Isolation and Purification of

FILE REFERENCE: 44149-3US1

CURRENT APPLICATION NUMBER: US/10/368,046

PRIOR FILING DATE: 2003-02-15

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,123

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,113

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,154

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,135

PRIOR FILING DATE: 2002-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 805

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein

US-10-368-046-9

Query Match 99.2%; Score 513; DB 4; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEWMLDQPEPTTDLXXXQUNDSEEDDEIDGPAQAEPRAHNYITVFCCK 60
Db 471 MGGDPTLHEWMLDQPEPTTDLGYEQUNDSEEDDEIDGPAQAEPRAHNYITVFCCK 530

Qy 61 CDSTRLCVQSTHVDIRLTEDLMGTGIVXPCISQKP 98
Db 531 CDSTRLCVQSTHVDIRLTEDLMGTGIVXPCISQKP 568

RESULT 7

US-10-367-367-9
Sequence 9, Application US/10367367
Publication No. US20040121465A1

GENERAL INFORMATION:

APPLICANT: Robin A. Robinson

TITLE OF INVENTION: Optimization of Gene Sequences of

FILE REFERENCE: 44149-2US1

CURRENT APPLICATION NUMBER: US/10/367,367

PRIOR FILING DATE: 2003-02-15

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 805

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein

US-10-367-367-9

Query Match 99.2%; Score 513; DB 4; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGGDPTLHEWMLDQPEPTTDLXXXQUNDSEEDDEIDGPAQAEPRAHNYITVFCCK 60
Db 471 MGGDPTLHEWMLDQPEPTTDLGYEQUNDSEEDDEIDGPAQAEPRAHNYITVFCCK 530

Qy 61 CDSTRLCVQSTHVDIRLTEDLMGTGIVXPCISQKP 98
Db 531 CDSTRLCVQSTHVDIRLTEDLMGTGIVXPCISQKP 568

RESULT 8
US-10-918-337-9

Sequence 9, Application US/10918337
Publication No. US20050118191A1

GENERAL INFORMATION:

APPLICANT: NOVAVAX, INC., et al.

TITLE OF INVENTION: Optimization of Gene Sequences of

FILE REFERENCE: 19065/2132

CURRENT APPLICATION NUMBER: US/10/918,337

PRIOR FILING DATE: 2004-08-13

PRIOR APPLICATION NUMBER: PCT/US03/04473

PRIOR FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: US 60/356,119

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,161

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,118

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,133

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,157

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,156

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,123

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: US 60/356,113

;; PRIOR FILING DATE: 2002-02-14
;; PRIOR APPLICATION NUMBER: US 60/356,154
;; PRIOR FILING DATE: 2002-02-14
;; Remaining Prior Application data removed - See file wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO: 9
;; LENGTH: 805
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
US-10-918-337-9

Query Match 99.2%; Score 513; DB 5; Length 805;
Best Local Similarity 96.9%; Pred. No. 1.9e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAPDRAHNYIVTFCK 60
Db 471 MHGDPPTLHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAPDRAHNYIVTFCK 530

Oy 61 CDSTLRLCVGSTHVDIRTLLEDLMGTGLGVXPCISQKP 98
Db 531 CDSTLRLCVGSTHVDIRTLLEDLMGTGLGVXPCISQKP 568

RESULT 9
US-09-728-466-1

;; Sequence 1, Application US/09728466
;; Patent No. US20010029022A1
;; GENERAL INFORMATION:

;; APPLICANT: Fisher, Christopher
;; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
;; FILE REFERENCE: 28341/6216
;; CURRENT APPLICATION NUMBER: US/09/728,466
;; CURRENT FILING DATE: 2000-12-01
;; PRIOR APPLICATION NUMBER: 09/382,616
;; PRIOR FILING DATE: 1999-08-25
;; NUMBER OF SEQ ID NOS: 43
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO: 1
;; LENGTH: 98
;; TYPE: PRT
;; ORGANISM: Papillomavirus sv1v1lag1
US-09-728-466-1

Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAPDRAHNYIVTFCK 60
Db 1 MHGDPPTLHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAPDRAHNYIVTFCK 60

Oy 61 CDSTLRLCVGSTHVDIRTLLEDLMGTGLGVXPCISQKP 98
Db 61 CDSTLRLCVGSTHVDIRTLLEDLMGTGLGVXPCISQKP 98

RESULT 10
US-09-820-765-4

;; Sequence 4, Application US/09820765
;; Publication No. US20020039584A1
;; GENERAL INFORMATION:

;; APPLICANT: BURGER, Alexander
;; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;; FORMULATIONS AND METHODS OF USE
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY & LARDNER

;; STREET: 3000 K Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20007-5109

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: IBM PC compatible
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/820,765
;; FILING DATE: 30-Mar-2001
;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/026,896
;; FILING DATE: 20-FEB-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Sandercock, Colin G.
;; REGISTRATION NUMBER: 31,298
;; REFERENCE/DOCKET NUMBER: 37067/102

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300
;; TELEFAX: (202) 672-5399
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 98 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1 MHGDPPTLHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAPDRAHNYIVTFCK 60
Db 1 MHGDPPTLHEYMLDQPEPTTDLXXYXQUNDSESEDEIDGPAGQAPDRAHNYIVTFCK 60

Oy 61 CDSTLRLCVGSTHVDIRTLLEDLMGTGLGVXPCISQKP 98
Db 61 CDSTLRLCVGSTHVDIRTLLEDLMGTGLGVXPCISQKP 98

RESULT 11
US-09-824-017-4

;; Sequence 4, Application US/09824017
;; Publication No. US20020197668A1
;; GENERAL INFORMATION:

;; APPLICANT: BURGER, Alexander
;; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
;; FORMULATIONS AND METHODS OF USE
;; NUMBER OF SEQUENCES: 28
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY & LARDNER
;; STREET: 3000 K Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20007-5109

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/824,017
;; FILING DATE: 03-Apr-2001
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEYMLDLPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHNYITFCCK 60
Db 1 MHGDTPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHNYITFCCK 60

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVPICSQKP 98
Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVPICSQKP 98

RESULT 12
US-09-986-118A-4
Sequence 4, Application US/09986118A
Publication No. US20030021806A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLER, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/986,118A
FILING DATE: 07-NO. US20030021806A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match 99.0%; Score 512; DB 3; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEYMLDLPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHNYITFCCK 60
Db 1 MHGDTPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHNYITFCCK 60

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVPICSQKP 98
Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVPICSQKP 98

RESULT 13
US-10-177-390-8
Sequence 8, Application US/10177390
Publication No. US20030143743A1
GENERAL INFORMATION:
APPLICANT: Schuler, Gerold
N.V. Antwerpse Innovatiecentrum
TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear
FILE REFERENCE: 021505wo/0h/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 98
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: fragment of
US-10-177-390-8

Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEYMLDLPETTDLYXXQLNDSSEDEIDGPAGQAEPPRAHNYITFCCK 60
Db 1 MHGDTPTLHEYMLDLPETTDLYCYEQLNDSSEDEIDGPAGQAEPPRAHNYITFCCK 60

Qy 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVPICSQKP 98
Db 61 CDSTRLCVOSTHVDIRLTEDLMGTGIVPICSQKP 98

RESULT 14
US-10-654-129-4
Sequence 4, Application US/10654129
Publication No. US20040081661A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLER, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
FILING DATE: 04-Sep-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-654-129-4

Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXOLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 60
Db 1 MHGDTPLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPRAHYNIIVTFCK 60

Qy 61 CDSTLRLCVQSTHVDIRLTEDLGMGTGIVXPICQKP 98
Db 61 CDSTLRLCVQSTHVDIRLTEDLGMGTGIVCPICQKP 98

RESULT 15
US-10-772-988-3
Sequence 3, Application US/10772988
Publication No. US20040139485A1
GENERAL INFORMATION:
APPLICANT: Thorngeltson, Snorri S.
APPLICANT: Woltach, Joseph T.
TITLE OF INVENTION: CDNA ENCODING A GENE BOG (B5T OVER-EXPRESSED GENE) AND ITS PROTEIN
FILE REFERENCE: 11613.29USW1
CURRENT APPLICATION NUMBER: US/10/772,988
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/09/637,746
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PCT/US99/04142
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: US 60/079,567
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 98
TYPE: PRT
ORGANISM: Human papillomavirus
US-10-772-988-3

Query Match 99.0%; Score 512; DB 4; Length 98;
Best Local Similarity 96.9%; Pred. No. 1.8e-53;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPLHEYMLDLPETTDLYXXYXOLNDSSEEDIDGPAGQAEPRAHYNIIVTFCK 60

Db 1 MHGDTPLHEYMLDLPETTDLYCYEQUNDSSSEEDIDGPAGQAEPRAHYNIIVTFCK 60
Qy 61 CDSTLRLCVQSTHVDIRLTEDLGMGTGIVXPICQKP 98
Db 61 CDSTLRLCVQSTHVDIRLTEDLGMGTGIVCPICQKP 98

Search completed: June 6, 2006, 12:32:59
Job time : 107.659 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 12:28:35 ; Search time 7.08434 Seconds

(without alignments)
159.985 Million cell updates/sec

Title: US-10-530-253-14

Sequence: 1 MHGPTTHHEVMDLPETTT.....LEDLMGTGIVPICSQKP 98

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Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*

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- 2: /EMC_Celerra_SIDS3/ptcdat/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptcdat/2/pubpaa/US07_NEW_PUB.pep:*
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- 5: /EMC_Celerra_SIDS3/ptcdat/2/pubpaa/PCr_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptcdat/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptcdat/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptcdat/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512	99.0	98	US-10-511-814-8	Sequence 8, Appli
2	511	98.8	98	US-10-511-814-11	Sequence 11, Appli
3	478	92.5	92	US-10-512-190-2	Sequence 2, Appli
4	102	19.7	21	US-11-209-206-6	Sequence 6, Appli
5	80.5	15.6	21	US-11-209-206-7	Sequence 7, Appli
6	62.5	12.1	148	US-11-293-697-2678	Sequence 2678, Ap
7	60.5	11.7	1287	US-10-505-928-341	Sequence 341, App
8	60	11.6	468	US-11-293-697-4473	Sequence 4473, App
9	58.5	11.3	462	US-10-953-349-39521	Sequence 39521, A
10	58.5	11.3	616	US-10-953-349-39520	Sequence 39520, A
11	58.5	11.3	646	US-10-953-349-39519	Sequence 39519, A
12	57.5	11.1	293	US-10-953-349-27425	Sequence 27425, A
13	57.5	11.1	266	US-10-953-349-27426	Sequence 27426, A
14	57.5	11.1	353	US-10-953-349-27424	Sequence 27424, A
15	57.5	11.1	446	US-10-953-349-39537	Sequence 39537, A
16	57.5	11.1	464	US-10-953-349-39536	Sequence 39536, A
17	57.5	11.1	499	US-10-953-349-3781	Sequence 3781, Ap
18	57.5	11.1	552	US-10-953-349-3780	Sequence 3780, Ap
19	57.5	11.1	618	US-10-953-349-39535	Sequence 39535, A
20	57	11.0	300	US-11-242-111-23	Sequence 23, Appli
21	57	11.0	314	US-09-981-845-1	Sequence 23, Appli
22	55.5	10.7	286	US-10-953-349-23406	Sequence 23406, A
23	55.5	10.7	293	US-10-953-349-23405	Sequence 23405, A
24	55.5	10.7	538	US-10-953-349-5452	Sequence 5452, Ap
25	55.5	10.7	544	US-10-953-349-5451	Sequence 5451, Ap

26	55.5	10.7	574	US-10-953-349-5450	Sequence 5450, Ap
27	55.5	10.7	878	US-10-468-193-32	Sequence 32, Appli
28	54.5	10.5	58	US-10-525-126-177	Sequence 177, App
29	54.5	10.5	58	US-10-525-126-215	Sequence 215, App
30	54.5	10.5	88	US-10-525-126-174	Sequence 174, App
31	54.5	10.5	88	US-10-525-126-175	Sequence 175, App
32	54.5	10.5	88	US-10-525-126-212	Sequence 212, App
33	54.5	10.5	88	US-10-525-126-213	Sequence 213, App
34	54.5	10.5	88	US-10-525-126-284	Sequence 284, App
35	54.5	10.5	88	US-10-525-126-299	Sequence 299, App
36	54.5	10.5	88	US-10-525-126-300	Sequence 300, App
37	54.5	10.5	255	US-10-953-349-20549	Sequence 20549, A
38	54.5	10.5	269	US-10-953-349-20548	Sequence 20548, A
39	54.5	10.5	489	US-11-293-697-2988	Sequence 2988, A
40	54	10.4	278	US-10-953-349-1526	Sequence 1526, App
41	54	10.4	323	US-10-518-414-1	Sequence 1, Appli
42	54	10.4	630	US-10-953-349-35808	Sequence 35808, A
43	54	10.4	676	US-10-953-349-35807	Sequence 35807, A
44	53.5	10.3	533	US-10-953-349-31198	Sequence 31198, A
45	53.5	10.3	639	US-10-953-349-23351	Sequence 23351, A

ALIGNMENTS

RESULT 1
US-10-511-814-8
; Sequence 8, Application US/10511814
; Publication No. US2006008472A1
; GENERAL INFORMATION:
; APPLICANT: McNamee, Dennis
; APPLICANT: Westbrook, Ili, Thomas F.
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.0016U2
; CURRENT APPLICATION NUMBER: US/10/511.814
; PRIOR FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12667
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
US-10-511-814-8
Query Match 99.0%; Score 512; DB 6; Length 98;
Best Local Similarity 96.9%; Pred. No. 2.4e-50;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGPTTHHEVMDLPETTTLYXXQLNDSSEBDEIDGAGQAEPPRAHNYITPCK 60
DB 1 MHGPTTHHEVMDLPETTTLYCYEQNLDSSEBDEIDGAGQAEPPRAHNYITPCK 60
QY 61 CDSTRLCVOSTHVDIRLTEDLLMGTTGIVPICSQKP 98
DB 61 CDSTRLCVOSTHVDIRLTEDLLMGTTGIVPICSQKP 98
RESULT 2
US-10-511-814-11
; Sequence 11, Application US/10511814
; Publication No. US2006008472A1
; GENERAL INFORMATION:
; APPLICANT: McNamee, Dennis
; APPLICANT: Westbrook, Ili, Thomas F.
; TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
; FILE REFERENCE: 21108.0016U2

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; CURRENT APPLICATION NUMBER: US/10/511,814
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US03/12667
; PRIOR FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: 60/374,245
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note =
US-10-511-814-11

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Query Match          98.8%; Score 511; DB 6; Length 98;
Best Local Similarity 95.9%; Pred. No. 3.1e-50;
Matches 94; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MHGDPPLHEHYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPPRAHNYITVFCCK 60
      1 MHGDPPLHEHYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPPRAHNYITVFCCK 60
Db      1 MHGDPPLHEHYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPPRAHNYITVFCCK 60
      1 MHGDPPLHEHYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPPRAHNYITVFCCK 60
Qy      61 CDSTLRLCVOSTHVDIRLTEDLMLGTGIVYPCISQKP 98
      61 CDSTLRLCVOSTHVDIRLTEDLMLGTGIVYPCISQKP 98
Db      61 CDSTLRLCVOSTHVDIRLTEDLMLGTGIVYPCISQKP 98
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RESULT 3
US-10-512-190-2
; Sequence 2, Application US/10512190
; Publication No. US20060099219A1
; GENERAL INFORMATION:
; APPLICANT: Hallee, Sophie
; APPLICANT: Burny, Arlene
; APPLICANT: Jacquuet, Alain
; APPLICANT: Bolten, Alex
; TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
; FILE REFERENCE: 9997.50USMO
; CURRENT APPLICATION NUMBER: US/10/512,190
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: PCT/BE03/000073
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 60/410,461
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: FR 0205173
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: FR 0304170
; PRIOR FILING DATE: 2003-04-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mutated (recombinant) HPV-16 E7
US-10-512-190-2

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Query Match          92.5%; Score 478; DB 6; Length 92;
Best Local Similarity 92.9%; Pred. No. 1.3e-46;
Matches 91; Conservative 0; Mismatches 1; Indels 6; Gaps 1;

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Qy      1 MHGDPPLHEHYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPPRAHNYITVFCCK 60
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Db      1 MHGDPPLHEHYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPPRAHNYITVFCCK 60
      1 MHGDPPLHEHYMLDLPETTDLYXXQLNDSSEEDRIDGPAQAEPPRAHNYITVFCCK 60
Qy      61 CDSTLRLCVOSTHVDIRLTEDLMLGTGIVYPCISQKP 98
      61 CDSTLRLCVOSTHVDIRLTEDLMLGTGIVYPCISQKP 98
Db      55 CDSTLRLCVOSTHVDIRLTEDLMLGTGIVYPCISQKP 92
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RESULT 4
US-11-209-206-6
; Sequence 6, Application US/11209206
; Publication No. US20060110794A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/11/209,206
; CURRENT FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early coding region of HPV 16
US-11-209-206-6

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Query Match          19.7%; Score 102; DB 7; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      27 QLNDSSEEDRIDGPAQAE 46
      27 QLNDSSEEDRIDGPAQAE 46
Db      2 QLNDSSEEDRIDGPAQAE 21
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RESULT 5
US-11-209-206-7
; Sequence 7, Application US/11209206
; Publication No. US20060110794A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/11/209,206
; CURRENT FILING DATE: 2005-08-22
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E7 early coding region of HPV 16
US-11-209-206-7

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Query Match          15.6%; Score 80.5; DB 7; Length 21;
Best Local Similarity 81.8%; Pred. No. 0.003;
Matches 16; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

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Qy      18 ETTDLYXXQLNDSSEEDRID 39
      18 ETTDLYXXQLNDSSEEDRID 39
Db      1 ETTDLYXXQLNDSSEEDRID 21
      1 ETTDLYXXQLNDSSEEDRID 21

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RESULT 6
US-11-293-697-2678
; Sequence 2678, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2678
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-2678

Query Match          12.1%; Score 62.5; DB 7; Length 148;
Best Local Similarity 30.6%; Pred. No. 2.5;
Matches 19; Conservative 5; Mismatches 21; Indels 17; Gaps 2;

QY 31 SSEEDDELIDGPAQAE-----DRAHNYIVTFCCKDSTLRLCVQSTHVDIR 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 50 SSSPESSSDGAGPEPTGSSGCTGSCSLSPVHSHMGMECP-----ILCCRSFHLHR 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 78 TL 79
DB 106 GL 107

RESULT 7
US-10-505-928-341
; Sequence 341, Application US/10505928
; Publication No. US20060086532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 341
; LENGTH: 1287
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-341

Query Match          11.7%; Score 60.5; DB 6; Length 1287;
Best Local Similarity 23.8%; Pred. No. 45;
Matches 19; Conservative 11; Mismatches 23; Indels 27; Gaps 3;

QY 23 YXXYQLNDSSEEDIDPA-----GOAEPDRAHNYIVTFCCKD 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1126 YGLQSSDSDSEDEPPDNADSKSEYLNQNLKSTPBDLGQCKERSKNDHETIN-CSNCE 1184
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 63 STLRLCVQSTHVDIRLTLEDL 82
DB 1185 SV-----GTNADTPVLNMI 1198

RESULT 8
US-11-293-697-4473
; Sequence 4473, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
```

```
; TITLE OF INVENTION: Novel full length CDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4473
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4473

Query Match          11.6%; Score 60; DB 7; Length 468;
Best Local Similarity 22.7%; Pred. No. 17;
Matches 29; Conservative 17; Mismatches 30; Indels 52; Gaps 7;

QY 16 QPETDLYXXYQLNDSSE-----EEDDELIDGPAQAE-----QAEP----- 47
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 35 EFQDLVLWPPRLNSSAEPQSLHSSRGVNNELPPQSGQGYGTRSRTPQSPHPTT 94
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 48 -----DRAHNYIVTFCCKDSTLRLCVQSTHVDIRLTLEDL-----WGLGIVXP 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 95 SSGNELPVVNSSASGNSCT--CNCSTLIQALIQ-----ELKTRKLMQIQAVGTQNRQDP 148
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 93 ---ICSQK 97
DB 149 ISLICSQR 156

RESULT 9
US-10-953-349-39521
; Sequence 39521, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39521
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-39521

Query Match          11.3%; Score 58.5; DB 6; Length 462;
Best Local Similarity 23.1%; Pred. No. 24;
Matches 24; Conservative 15; Mismatches 30; Indels 35; Gaps 5;

QY 6 PTLERMYLDLOPETDLYXXYQLNDSSE---ED-----EIDGPAQAEPPRAHNYI 54
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 351 PAVHMASYDLGKAXYDV-----LRONSRRFLLEVDYRNPGPLQEGFGADSKP----- 398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 55 VTFCKCDSTLRLCVQSTHV--DIRLTEDLMTGLGIVXPICSQ 96
DB 399 -----ISLCEVDODYGRIRKLOEYILEKYSIVKPCSQ 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-10-953-349-39520
; Sequence 39520, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
```

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; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 39520
; LENGTH: 616
; TYPE: PR1
; ORGANISM: Zsa mayas subsp. mayas
US-10-953-349-39520

```

Query Match	11.3%	Score 58.5	DB 6	length 616
Best Local Similarity	23.1%	Pred. No. 33		
Matches 24	Conservative 15	Mismatches 30	Indels 35	Gaps 5

```
Oy      6 PTLEHYMLDQAPETTLXYXQLNDSEEE---ED-----EIDGAGQAEDRAHANI    54
          .|.:.|.|.:|.:.|||               |.|.|.|.:.|..|
DbB     505 PAVNHAASVDLGGKAYDV----LRQNSSRFLEDVYRNPGPLPFGEPADSKF-----   552
```

```
QY 55 VTFCCKDSTLRLCVQSTHV--DIRTEDLMTGLGIKVPISQ 96
      : ||| : | : | | | |
Db 553 -----ISLCVEDQDPYMGRIKKLQYLELKVKSIVKPGSQ 586
```

```

RESULT 11
US-10-953-349-39519
: Sequence 39519, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US-10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 39519
:
: LENGTH: 646
:
: TYPE: PRT
: ORGANISM: Zea mays subsp. mays
US-10-953-349-39519

```

Query Match	11.3%	Score 58.5;	DB 6;	Length 646;
Best Local Similarity	23.1%	Pred. No. 35;		
Matches	24;	Conservative 15;	Mismatches 30;	Indels 35; Gaps 5
Qy	6	PTLEHYMLDQPEETLDDXXYYQANLSSSE---	ED-----	EIDRPGAQAEPPRAHNI 54
	:	:	:	:
Db	535	PAYMASTADYLGKAYDV----	LRONSSRFLEIDYRNPNGPQLQFGPADSK	----- 582
Qy	55	VTFCCKCDSTLRLCYQSTHV--	DIPTLEDLLMGLTGLVXPICSQ	96
	:	:	:	:
Db	583	-----ISLCEVDODVYGRIRKQLQEYLEKXKSIYKPGCSQ		616

```

RESULT 12
US-10-953-349-27426
: Sequence 27426, Application US/10953349
: Publication No. US20060107345A1
: GENERAL INFORMATION:
: APPLICANT: ALEXANDROV, Nickolai et al.
: TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
: TITLE OF INVENTION: ENCODED THERBY
: FILE REFERENCE: 2750-1579PUS2
: CURRENT APPLICATION NUMBER: US/10/953,349
: CURRENT FILING DATE: 2004-09-30
: NUMBER OF SEQ ID NOS: 40252
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 27426
: LENGTH: 233
: TYPE: PRT
: ORGANISM: Triticum aestivum
: US-10-953-349-27426

```

	Query Match	11.1%	Score 57.5;	DB 6;	Length 233;
	Best Local Similarity	27.6%	Pred. No. 15;		
	Matches	16;	Conservative	11;	Mismatches 24; Gaps 7;
Qy	8 LHEYML-DLQETDITLYXXOXNDSSSEEDIDEGACGAEDDPAAHYNNVTFCKCKDST	64			
Dd	85 IQSYVLGSDPADDAVDADHNTTSISADDHYKD-----TSKRYHHAYHTNGTVCDDL	136			

```

RESULT 13
US-10-953-349-27425
; Sequence 27425, Application US/10953349
; Publication No. US20060107345M1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PU52
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 27425
;
; LENGTH: 296
;
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-27425

```

Query Match	11.1%	Score 57.5	DB 6	Length 296
Best Local Similarity	27.6%	Pred. No. 19		
Matches	16	Conservative	11	Mismatches 24; Indels 7; Gaps 2;
QY	8	LHEVWL-DLQETTDLLXXYXQANDSSEBEDEIDGPGAGAEEDRHHVNIIVFCKCDST	64	
DB	148	IOEVLGSEYDDADDAVYHNDHTSSAEDHYKD-----TSKRHHVNYITGVCDDL	139	

```

RESULT 14
US-10-953-349-27424
; Sequence 27424, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27424
;
; LENGTH: 353
;
; TYPE: PRT
;
; ORGANISM: Trilicium aestivum
US-10-953-349-27424

```

```

Query Match Similarity 11.1%; Score 57.5; DB 6; Length 353;
Best Local Similarity 27.6%; Pred. No. 23;
Matches 16; Conservative 11; Mismatches 24; Indels 7; Gaps 2;

QY      8 LHEVYL-DLQPEETDLYXXQLNDSSEBEEDIDGPAQAEPDRAHYNIVTFCCKDST 64
      :|::||::||::||::||::||::||::||::||::||::||::||::||
Db      205 IQEYVLGGYDPDADYADYHNDHTSESADEDHYKD-----TSKRHYVHYVTNGTCDLT 256

RESULT 15
US-10-953-349-39537
; Sequence 39537, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY

```

FILE REFERENCE: 2750-1579PUS2
 CURRENT APPLICATION NUMBER: US/10/953,349
 CURRENT FILING DATE: 2004-09-30
 NUMBER OF SEQ ID NOS: 40252
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 39537
 LENGTH: 446
 TYPE: PRT
 ORGANISM: Zea mays subsp. mays
 US-10-953-349-39537

Query Match 11.1%; Score 57.5; DB 6; Length 446;
 Best Local Similarity 23.8%; Pred. No. 30;
 Matches 24; Conservative 15; Mismatches 33; Indels 29; Gaps 4;

OY 6 PTLHEVMDLQPETTDLYXXQLNDSSEED-----EIDGPAGQAEPPRAHYNIYTF 57
 Db 333 PAVHMASVDLKGKAYDV--LRQNSSSFLLEDVYRNPGPLQFEGPGADSKP----- 380
 OY 58 CCKCDSTLRLCVQSTHV--DIRTLEDLMGTIGIVXPICSQ 96
 Db 381 -----ISLCVBDQDYMGRIKQLQBYLEKVRIVPGCSQ 414

Search completed: June 6, 2006, 12:33:22
 Job time : 7.08434 secs

This Page Blank (uspto)

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OM protein - protein search, using ew model

Run on: June 6, 2006, 12:05:01 ; Search time 18.8916 Seconds

(without alignments)
499.124 Million cell updates/sec

Title: US-10-530-253-14

Perfect score: 517
Sequence: 1 MHGDTPTLHEVMDLPETTT.....LEDLMDGTGIVXPICSOXP 98Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	99.0	98	1	W7MLHS E7 protein - human
2	381.5	73.8	99	1	W7MLJ35 E7 protein - human
3	372	72.0	98	1	W7MLJ31 E7 protein - human
4	295	57.1	97	1	W7MLJ33 E7 protein - human
5	294	56.9	99	2	S36574 E7 protein - human
6	288.5	56.0	98	1	W7ML58 E7 protein - human
7	245	47.4	98	1	W7ML11 E7 protein - human
8	243	47.0	98	1	W7ML6 E7 protein - human
9	222.5	43.0	97	2	S36516 E7 protein - human
10	218.5	42.3	113	1	W7MLR1 E7 protein - human
11	213	41.2	106	2	S36562 E7 protein - human
12	209.5	40.5	105	2	S36504 E7 protein - human
13	208.5	40.3	105	2	S36528 E7 protein - human
14	200.5	38.8	101	1	W7MLJ3 E7 protein - human
15	200.5	38.8	105	1	W7ML18 E7 protein - human
16	194	37.5	98	1	W7MLC1 E7 protein - human
17	183.5	35.5	93	1	W7ML42 E7 protein - human
18	183.5	35.5	105	2	B44890 E7 protein - human
19	178.5	34.5	92	1	S15622 E7 protein - human
20	178.5	34.5	105	2	S36580 E7 protein - human
21	178.5	34.5	111	2	S36585 E7 protein - human
22	178	34.4	101	1	W7ML51 E7 protein - human
23	175.5	33.9	92	1	S15615 E7 protein - human
24	173.5	33.6	86	2	S36533 E7 protein - human
25	170	32.9	95	2	S36480 E7 protein - human
26	170	32.9	109	1	W7ML39 E7 protein - human
27	169	32.7	104	2	S36510 E7 protein - human
28	166.5	32.2	92	2	S36498 E7 protein - human
29	157.5	30.5	110	1	W7MLPR E7 protein - human

30	150.5	29.1	111	2	S36556 E7 protein - human
31	148	28.6	93	2	S36474 E7 protein - human
32	140.5	27.2	104	2	S36545 E7 protein - human
33	138	26.7	93	1	W7ML E7 protein - human
34	122	23.6	93	2	S36591 E7 protein - human
35	120.5	23.3	102	2	S36492 E7 protein - human
36	119	23.0	103	2	S36539 E7 protein - human
37	116.5	22.5	102	2	S36486 E7 protein - human
38	113	21.9	103	1	W7ML47 E7 protein - human
39	112	21.7	103	1	W7ML5 E7 protein - human
40	109	21.1	103	1	W7MLB5 E7 protein - human
41	105	20.3	103	1	W7ML8 E7 protein - human
42	87	16.8	94	1	W7MLB E7 protein - human
43	83.5	16.2	98	2	B61399 E7 protein - human
44	80	15.5	55	2	S19907 E7 protein - human
45	79.5	15.4	98	2	A61399 E7 protein - human

ALIGNMENTS

RESULT 1

W7MLHS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

W7ML35
E7 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: F40824; S36522
R:Marich, J.E.; Ponteler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: F40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-99 <MBR>
A:Cross-references: UNIPROT:P27230; UNIPARC:UPI000000035E; GB:M74117; NID:G333050; PIDN:
R:DeLune, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36522
A:Accession: S36522
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99
A:Cross-references: UNIPARC:UPI000000035E; EMBL:X74477; NID:G396397; PIDN:CAA52562.1; PI
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-95/Region: zinc finger CCCC motif

Query Match 73.8%; Score 381.5; DB 1; Length 99;
Best Local Similarity 73.5%; Pred. No. 2.2e-35;

Matches 72; Conservative 11; Mismatches 14; Indels 1; Gaps 1;

Oy 1 MHGPTLHEMYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 59
Db 1 MHGPTLHEMYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 60
Oy 60 KCDSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 97
Db 61 KCDSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 98

RESULT 3

W7ML31

E7 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: B32444
R:Goldaborough, M.D.; Dislyvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: B32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <COL>
A:Cross-references: UNIPROT:P17387; UNIPARC:UPI000013840A; GB:J04353; NID:G333048; PIDN:
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 72.0%; Score 372; DB 1; Length 98;
Best Local Similarity 71.1%; Pred. No. 2.5e-34;

Matches 69; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Oy 1 MHGPTLHEMYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 60
Db 1 MHGPTLHEMYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 60
Oy 61 CDSSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 97
Db 61 CDSSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 97

Db 61 CKSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 97

RESULT 4

W7ML33

E7 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03689; S23831; S23827
R:Coie, S.T.; Streck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, with
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03689
A:Molecule type: DNA
A:Residues: 1-97 <COL>
A:Cross-references: UNIPROT:P06429; UNIPARC:UPI000013840C; GB:M12732; NID:G333049; PIDN:
R:Smijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
submitted to the EMBL Data Library, January 1992
A:Description: HPV type 33 in a consillar carcinoma generates its putative E7 mRNA via tr
A:Reference number: S39906
A:Accession: S3831
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97 <SN1>
A:Cross-references: UNIPARC:UPI000013840C; EMBL:X64085; NID:G60278; PIDN:CAA45434.1; PID
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 57.1%; Score 295; DB 1; Length 97;
Best Local Similarity 57.7%; Pred. No. 9.4e-26;

Matches 56; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

Oy 1 MHGPTLHEMYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 60
Db 1 MRGHKPTLKEVYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 60
Oy 61 CDSSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 97
Db 61 CDSSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 97

RESULT 5

S36574

E7 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S36574
R:DeLune, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36574
A:Molecule type: DNA
A:Residues: 1-99
A:Cross-references: UNIPROT:P36831; UNIPARC:UPI000013841C; EMBL:X74481; NID:G397038; PIDN:
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match 56.9%; Score 294; DB 2; Length 99;
Best Local Similarity 57.1%; Pred. No. 1.2e-25;

Matches 56; Conservative 17; Mismatches 23; Indels 2; Gaps 1;

Oy 1 MHGPTLHEMYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 58
Db 1 MRGHKPTLKEVYLDLQPTTDLXXYXQUNDSS-EEDEIDGPAGAEPPRAHNYITFCCK 60
Oy 59 CKDSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 96
Db 61 HSDSTLRICVOSTHVDIRTLBDMGLTGIVXPICSO 98

RESULT 6

W7ML58

E7 protein - human papillomavirus type 58

C:Species: human papillomavirus type 58

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: F36779

R:Kiril, Y.; Iwamoto, S.; Matsukura, T.

Virology 185, 424-427, 1991

A:Title: Human papillomavirus type 58 DNA sequence.

A:Reference number: A36779; MUID:92024102; PMID:1656594

A:Accession: F36779

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-58 <KIR>

A:Cross-references: UNIPROT:P26557; UNIPARC:UPI000000344B; GB:D90400; NID:G222386; PIDN:

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-95/Region: zinc finger CCCC motif

Query Match 56.0%; Score 289.5; DB 1; Length 98;

Best Local Similarity 57.1%; Pred. No. 3.9e-25;

Matches 56; Conservative 16; Mismatches 25; Indels 1; Gaps 1;

QY 1 MHGDPPTHEWMLDQPEPTDLYXXQOLNDSSEED-DEIDGPAQAEPDRAHNIIVTFC 59

DB 1 MGNPPTREYILDHPETDLCYEQQLDSSDEDEIGDGPQAPATANYIVTCCY 60

QY 60 KCDSTLRVCVOSTHVDIRTLLEDLMGTGIYXPCISOK 97

DB 61 TCGTIVRLCINSTTDTVRLQQLMGTCITVPCSAQ 98

RESULT 7

W7ML1

E7 protein - human papillomavirus type 11

C:Species: human papillomavirus type 11

C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004

C:Accession: A03690

R:Datmann, K.; Schwarz, E.; Giesmann, L.; zur Hausen, H.

Virology 151, 124-130, 1986

A:Title: The nucleotide sequence and genome organization of human papilloma virus type 1

A:Reference number: A03690; MUID:86181601; PMID:3008427

A:Accession: A03690

A:Molecule type: DNA

A:Residues: 1-98 <DAR>

A:Cross-references: UNIPROT:P04020; UNIPARC:UPI00001383F7; GB:M14119; NID:G333026; PIDN:

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 47.4%; Score 245; DB 1; Length 98;

Best Local Similarity 53.0%; Pred. No. 3.5e-20;

Matches 53; Conservative 14; Mismatches 29; Indels 4; Gaps 3;

QY 1 MHGDPPTHEWMLDQ-PEPTDLYXXQOLNDSSEED-DEIDGPAQAEPDRAHNIIVTFC 58

DB 1 MHGRLVTKDVLIDQPPDPVGLHCYEQLEDSEBEVKVD--KODAPLITQHYILTCC 58

QY 59 CKDSTLRVCVOSTHVDIRTLLEDLMGTGIYXPCISOK 98

DB 59 CGCDSNRLVVECTDGTIRQLDGLGLTINIVCPICAPK 98

RESULT 8

W7ML6

E7 protein - human papillomavirus type 6b

C:Species: human papillomavirus type 6b

C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C:Accession: D20558

R:Schwarz, E.; Duzic, M.; Demankowski, C.; Laternmann, O.; Zech, R.; Wolfepberger, E.; Su

EMBO J. 2, 2341-2348, 1983

A:Title: DNA sequence and genome organization of genital human papillomavirus type 6b.

A:Reference number: A09075; MUID:84131949; PMID:6321162

A:Accession: D20558

A:Molecule type: DNA

A:Residues: 1-98 <SCH>

A:Cross-references: UNIPROT:P06464; UNIPARC:UPI0000138429; GB:X00203; NID:G60955; PIDN:

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 47.0%; Score 243; DB 1; Length 98;

Best Local Similarity 52.5%; Pred. No. 5.9e-20;

Matches 52; Conservative 15; Mismatches 28; Indels 4; Gaps 3;

QY 1 MHGDPPTHEWMLDQ-PEPTDLYXXQOLNDSSEED-DEIDGPAQAEPDRAHNIIVTFC 58

DB 1 MHGRLVTKDVLIDQPPDPVGLHCYEQLEDSEBEVKVD--DSQPLKQHFQIVTCC 58

QY 59 CKDSTLRVCVOSTHVDIRTLLEDLMGTGIYXPCISOK 97

DB 59 CGCDSNRLVVECTDGTIRQLDGLGLTINIVCPICAPK 97

RESULT 9

S36516

E7 protein - human papillomavirus type 34

C:Species: human papillomavirus type 34

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36516

R:Dejiliu, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36516

A:Molecule type: DNA

A:Residues: 1-97

A:Cross-references: UNIPROT:P36828; UNIPARC:UPI000013840D; EMBL:X74476; NID:G396989; PIR

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 43.0%; Score 222.5; DB 2; Length 97;

Best Local Similarity 49.0%; Pred. No. 1.1e-17;

Matches 48; Conservative 18; Mismatches 29; Indels 3; Gaps 3;

QY 1 MHGDPPTHEWMLDQPEPTDLYXXQOLNDSSEED-DEIDGPAQAEPDRAHNIIVTFC 59

DB 1 MHGKPSVQDVLIDKPTERTDLCYESTL-DNSEDEDTDSHL-ERQEQAWYRVTPDS 58

QY 60 KCDSTLRVCVOSTHVDIRTLLEDLMGTGIYXPCISOK 97

DB 59 KQSTVCLTSTHADVLELDMGALKIVCPNCSRR 96

RESULT 10

W7ML1

E7 protein - rhesus papillomavirus (type 1)

C:Species: rhesus papillomavirus

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: B38503

R:Ostrow, R.S.; Labresh, K.V.; Faras, A.J.

Virology 181, 424-429, 1991

A:Title: Characterization of the complete Rhyv 1 genomic sequence and an integration loc

A:Reference number: A38503; MUID:91135018; PMID:1847267

A:Accession: B38503

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-113 <OST>

A:Cross-references: UNIPROT:P22161; UNIPARC:UPI000013842F; EMBL:M37717

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation

Query Match 42.3%; Score 218.5; DB 1; Length 113;

Best Local Similarity 43.8%; Pred. No. 3.7e-17;

Matches 49; Conservative 13; Mismatches 35; Indels 15; Gaps 2;

Oy 1 MHGDTPTLHETMIDL----QPETDLDLYXXYNOLDSSEEDETIDGPAGAEPRAH----- 51
Db 1 MIGKPKLTIEDVLDLPFPQPDPVDLMCKEGLSSSDEBDEDHHNNNQOHHOHAREEV 60

Oy 52 -----YIVTFCCCKDSTLRLCVGOSTHVDRTRTEDLMTGTIGTYXPICSOK 97
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|||
Db 61 PEDGGCTRVSDCYSCGKPRLRWVSSHHEURLVEDLMLTGTDLVCPSCASR 112

RESULT 11
S36562
E7 protein - human papillomavirus type 45
C/Species: human papillomavirus type 45
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36562
R/Dellus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36562
A/Molecule type: DNA
A/Residues: 1-106
A/Cross-references: UNIPROT:P21736; UNIPARC:UPI0000138416; ENBL:X74479; NID:g397022; PIRSI:
Superfamily: papillomavirus E7 protein
Keywords: DNA binding; early protein; transcription regulation

```

Query Match          41.2%; Score 213; DB 2; Length 106;
Best Local Similarity 43.8%; Pred. No. 1,4e-16;
Matches 46; Conservative 15; Mismatches 32; Indels 12; Gaps 3;

OY 1 MHGDPPTLHEWMLDOPET-----TDLYXXYXQLNDSSEEDSIDG-----PAGQAEPPRA 50
Db 1 MHGRETITQELVHLHPQNEIDPPVDLICYEDLSSEEDNEADGVSHQLPARAEFOR- 59
OY 51 HNYIVTFCCCKDSTLRLCVOSTHVDIRTEEDLLMGTIGIYXPICS 95
Db 60 -HKLVCVCKCDGRILFVTESSAEEDRLTQOLFSTLSFVCPWCA 103

RESULT 12
S36504
E7 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36504
R:Delius, H.; Holmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36504
A:Molecule type: DNA
A:Residues: 1-105 <DEL>
A:Cross-references: UNIPROT:P36826; UNIPARC:UP10000138409; EMBL:X74474; NID:g396973; PIR
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation

Query Match          40.5%; Score 209.5; DB 2; Length 105;
Best Local Similarity 45.2%; Pred. No. 3.5e-16;
Matches 47; Conservative 17; Mismatches 33; Indels 7; Gaps 4;

OY 1 MHGDPPTLHEWMLDOPET-TDLYXXYXQLNDSSE-EDSIDG---PAGQAEPPRAH--YN 53
Db 1 MHGAVTTIPETIIDLVPQTEITDLHCYEQANSSEDEDEVDNLOKQOQARQEGHCYTL 60
OY 54 IVTFCCCKDSTLRLCVOSTHVDIRTEEDLLMGTIGIYXPICSQK 97
Db 61 INFOCCRCASAVQLAVOSPTEKELRALQOMLGALEIVCPLCATR 104

RESULT 13
S36528
S37 protein - human papillomavirus type 53

```

C1Species: human papillomavirus type 53
C1Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C1Accession: S36528
R1Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A1Description: Primer-directed sequencing of human papillomavirus types.
A1Reference number: S36469
A1Accession: S36528
A1Molecule type: DNA
A1Residues: 1-105
A1Cross-references: UNIPROT:P36832; UNIPARC:UPI0000013841D; EMBL:X74482; NID:g397046; PID:
C1Superfamily: papillomavirus E7 protein
C1Keywords: DNA binding; early protein; transcription regulation

Query Match	40.3%;	Score 208.5;	DB 2;	Length 105;
Best Local Similarity	43.3%;	Pred. No. 4.5e-16;		
Matches	45;	Conservative 23;	Mismatches 29;	Indels 7;
			Gaps 4;	
QY	1	MHGDPPTLHENVLDLPET-TDLYXXQLNDS-SEDEDEID----	GPAGQAEPDAAH--YN	53
Db	1	MHGAVPTLPQYXIEILPQTEIDLQCHEQLNDSSEDEDEDEVDHLOEQPQARRBQHCYCL		60
QY	54	IVTFCCKDSTRLCVOSTHVDIRLTLEDLMGTGLVXPICSQK		97
Db	61	LETQCCRESIVLQAVQSSSTKEIRLQOMLGMVETLVCPLCAATR		104

RESULT 14

W7ML13
E7 protein - human papillomavirus type 13.
C:Species: human papillomavirus type 13
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: B42955
R:van Ransst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G
Virology 190, 587-596, 1992
A:Title: Human papillomavirus type 13 and pYGMV chimpanzee papillomavirus type 1: Compar
A:Reference number: A42955; MUID:92391075; PMID:132567
A:Accession: B42955
A:Molecule type: DNA
A:Residues: 1-101 <MAN>
A:Cross-references: UNIPROT:002271; UNIPARC:UP100001383F9; EMBL:X62843; NID:G60295; PIDN
A:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:61-97/Region: zinc finger CCCC motif

```
Query Match      38.8%; Score 200.5; DB 1; Length 101;
Beat Local Similarity 44.7%; Pred.No.3.3e-15;
Match     46; Conservative   13; Mismatches 35; Indels 9; Gaps 2;

Oy      1 MHGDPPTLHEVWLADLPETTDLYXXYQLNDSSEEDDEIGPAGQAEPRAH-----YNI 54
        ||| |::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       1 MHGKRTPLKDYLLELTTPDVGHLCHNQLDSS---EDEVEBQAQNQGATGHSTLLCYOI 57
        ||| |::||::||::||::||::||::||::||::||::||::||::||::||

Oy      55 VTFCCKCDSTLRLCVQSTHVDIRITLEDILMGTLGIYXPICSOK 97
        :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db       58 LTSCSKCCSNVRLVVECTGPDIHDHDLTGTLINIVCPICAPK 100
        ::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 15
w7WtLI8
E7 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #ext_change 09-Jul-2004
C:Accession: B26165; H26251
R:Siedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A>Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: B26165
A:Molecule type: DNA
A:Residues: 1-105 <SEQ>
A:Cross-references: UNIPROT:P06788; UNIPARC:UPI0000000DB5; GB:X04773; NID:g60876; PIDN:CI
```

R: Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
A: Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1
A: Reference number: A92937; MUID: 87283682; PMID: 3039146
A: Accession: H26251
A: Molecule type: DNA
A: Residues: 1-105 <COL>
A: Cross-references: UNIPARC:UPI00000000B5; GB:X05015; NID:G60975; PIDN:CAA28665.1; PID:G
C: Superfamily: Papillomavirus E7 protein
C: Keywords: DNA binding; early protein; transcription regulation
Query Match 38.8%; Score 200.5; DB 1; Length 105;
Best Local Similarity 39.6%; Pred. No. 3.5e-15;
Matches 42; Conservative 20; Mismatches 33; Indels 11; Gaps 3;
QY 1 MHGDTPTLHEYMLDLPET--TDLVXXYQLNDSSEDEIDG-----PAGQAEPPRAH 51
DB 1 MHGPRATLDIVLHLEPQWEIPVDLLCHEQLSDSEBENDEIDGVNHHLPARRAEPR-- 58
QY 52 YNIVTFCKCKDSTLRLCYOSTHVDIRITLEDLMGTLGIYXPTCSOK 97
DB 59 HTMLCMCKCKCEARIELVNESSADDLRAFOQLFLNTLSFVCPWCASQ 104

Search completed: June 6, 2006, 12:11:54
Job time : 18.8916 secs

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 11:58:34 ; Search time 151.133 Seconds
(without alignments)
599.815 Million cell updates/sec

Title: US-10-530-253-14
Perfect score: 517
Sequence: 1 MHGDPPTLHEVWLQDPERT.....LEDLMGTGLGVXPICGQKP 98

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2:*
1: uniprot_sprot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512	99.0	98	1	VE7_HPV16
2	512	99.0	98	2	054788_HPV16
3	512	99.0	98	2	Q778G4_HPV16
4	512	99.0	98	2	Q778G6_HPV16
5	512	99.0	98	2	Q778G8_HPV16
6	512	99.0	98	2	Q778G9_HPV16
7	512	99.0	98	2	Q778H1_HPV16
8	512	99.0	98	2	Q778H2_HPV16
9	512	99.0	98	2	Q778H7_HPV16
10	512	99.0	98	2	Q778H9_HPV16
11	512	99.0	98	2	Q778I0_HPV16
12	512	99.0	98	2	Q778I1_HPV16
13	512	99.0	98	2	Q778I3_HPV16
14	512	99.0	98	2	Q778I5_HPV16
15	512	99.0	98	2	Q778I7_HPV16
16	512	99.0	98	2	Q778I9_HPV16
17	508	98.3	98	2	Q12337_HPV16
18	507	98.1	98	2	Q11650_HPV16
19	507	98.1	98	2	Q778H3_HPV16
20	507	98.1	98	2	Q778H5_HPV16
21	507	98.1	98	2	Q6GRD2_HPV16
22	507	98.1	98	2	Q6GRD3_HPV16
23	507	98.1	98	2	Q2MJ74_HPV16
24	504	97.5	98	2	Q12338_HPV16
25	500	96.7	98	2	Q8V1J0_HPV16
26	499	96.5	98	2	Q6GRD4_HPV16
27	486	94.0	94	2	Q8B5P6_HPV16
28	478	92.5	93	2	Q9QDH6_HPV16
29	477	92.3	93	2	Q9QDH2_HPV16
30	477	92.3	93	2	Q9QDH4_HPV16
31	477	92.3	93	2	Q9QDH8_HPV16

32	406	78.5	77	2	Q8B5P5_9PAPI	Q8B5P5 human papil
33	381.5	73.8	99	1	VE7_HPV35	P22730 human papil
34	381.5	73.8	99	2	Q76WP2_9PAPI	Q76WP2 human papil
35	372	72.0	98	1	VE7_HPV31	P17387 human papil
36	367	71.0	98	2	Q6T377_HPV31	Q6T377 human papil
37	343	66.3	65	2	Q8B5G3_9PAPI	Q8B5G3 human papil
38	316	61.1	99	2	Q90724_HPV67	Q90724 human papil
39	295	57.1	97	1	VE7_HPV33	P06429 human papil
40	294	56.9	99	1	VE7_HPV52	P36831 human papil
41	289.5	56.0	98	1	VE7_HPV58	P26557 human papil
42	289.5	56.0	98	2	Q547M4_HPV58	Q547M4 human papil
43	288.5	55.8	98	2	Q9QCZ1_HPV58	Q9QCZ1 human papil
44	286.5	55.4	98	2	Q8QSF0_HPV58	Q8QSF0 human papil
45	285.5	55.2	98	2	Q8QHN7_HPV58	Q8QHN7 human papil

ALIGNMENTS

RESULT 1
VE7_HPV16
AC VE7_HPV16 STANDARD; PRT; 98 AA.
ID P03129;
DT 21-JUL-1966, integrated into UniProtKB/Swiss-Prot.
DT 21-JUL-1966, sequence version 1.
DT 07-FEB-2006, entry version 43.
DE Protein E7.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBITaxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Roweckamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnaut G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-V cells, a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Torresello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=Isolate African 1, and isolate European German 131;
RA Terai M., Fu L., Ma Z., Burk R.D.;
RT "Cloning and sequencing of non-European human papillomavirus (HPV) variant complete genomes from cervicovaginal cells by an overlapping PCR method.";
RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and transformation functions similar to those of adenovirus E1A.";
CC Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating activities.
CC -!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more often associated with malignant genital cancers in humans.

CC -1- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivative License
CC -----
DR EMBL: K02718; AAA46940.1; -; Genomic DNA.
DR EMBL: D00735; BAA00633.1; -; Genomic DNA.
DR EMBL: U76411; AAB18962.1; -; Genomic DNA.
DR EMBL: U76412; AAB18963.1; -; Genomic DNA.
DR EMBL: U76413; AAB18964.1; -; Genomic DNA.
DR EMBL: AF003020; AAB70737.1; -; Genomic DNA.
DR EMBL: AF003023; AAB70740.1; -; Genomic DNA.
DR EMBL: AF003024; AAB70741.1; -; Genomic DNA.
DR EMBL: AF003025; AAB70742.1; -; Genomic DNA.
DR EMBL: AF003026; AAB70743.1; -; Genomic DNA.
DR EMBL: AF536179; AAO10713.1; -; Genomic DNA.
DR EMBL: AF536180; AAO10721.1; -; Genomic DNA.
DR PIR: A03688; W7MLHS.
DR InterPro: IPR000148; Papv_E7.
DR Pfam: PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Transcription;
KW Transcription regulation.
FT CHAIN 1
FT MOTIF 58 61 /FtId=PRO_0000133414.
FT MOTIF 91 94 C-XX-C motif-1.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
Query Match 99.0%; Score 512; DB 1; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHEYMADLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
DB 1 MHGDTPTLHEYMADLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRLTEDLLMGTLGIYXPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRLTEDLLMGTLGIYXPCISQKP 98
RESULT 2
Q547B8 HPV16 PRELIMINARY; PRT; 98 AA.
AC Q547B8;
DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 24-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang, J., Gao, Y., Yan X.;
RT "Cloning and sequence analysis of Human papillomavirus type 16 E7 gene
in China.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: AF512012; AAM74160.1; -; Genomic DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHEYMADLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
DB 1 MHGDTPTLHEYMADLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRLTEDLLMGTLGIYXPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRLTEDLLMGTLGIYXPCISQKP 98
RESULT 3
Q778G4 HPV16 PRELIMINARY; PRT; 98 AA.
AC Q778G4;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
RL J. Gen. Virol. 81:317-325(2000).
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CC -----
DR EMBL: AJ388069; CAB45131.1; -; Genomic DNA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0003700; F:transcription factor activity; IEA.
DR GO: GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro: IPR000148; Papv1_E7.
DR Pfam: PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MHGDTPTLHEYMADLOPETTDLYXXQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
DB 1 MHGDTPTLHEYMADLOPETTDLYCYEQLNDSSEDEIDGPAQAEPDRAHYNIVTFCK 60
QY 61 CDSTLRFCVOSTHVDIRLTEDLLMGTLGIYXPCISQKP 98
DB 61 CDSTLRFCVOSTHVDIRLTEDLLMGTLGIYXPCISQKP 98
RESULT 4
Q778G6 HPV16 PRELIMINARY; PRT; 98 AA.
AC Q778G6;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=20112892; PubMed=10644829;
RX van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

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RT Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RA "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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CC
CC -----
DR EMBL, AJ388068; CAB5129.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 98
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
SQ
SQ
Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0
Qy 1 MHGDTPTLHEYMLDLPETDTLXXYYXQNDSSSEEDDEIDPGAQAEPPRAHNYITPCK 60
Db 1 MHGDTPTLHEYMLDLPETDTLXXYYXQNDSSSEEDDEIDPGAQAEPPRAHNYITPCK 60
Qy 61 CDSTLRLCVOSTHYDRIRTLEDLNGTIGIYVPICSQKP 98
Db 61 CDSTLRLCVOSTHYDRIRTLEDLNGTIGIYVPICSQKP 98
Qy
Db
RESULT 5
Q778G8_HPV16
AC Q778G8_HPV16 PRELIMINARY; PRT; 98 AA.
ID Q778G8_HPV16
AC Q778G8;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_Taxid=3333760;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
CC
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CC
CC -----
DR EMBL, AJ388067; CAB5127.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR NON_TER 98
FT SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
SQ
SQ
Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0
Qy 1 MHGDTPTLHEYMLDLPETDTLXXYYXQNDSSSEEDDEIDPGAQAEPPRAHNYITPCK 60
Db 1 MHGDTPTLHEYMLDLPETDTLXXYYXQNDSSSEEDDEIDPGAQAEPPRAHNYITPCK 60
Qy 61 CDSTLRLCVOSTHYDRIRTLEDLNGTIGIYVPICSQKP 98
Db 61 CDSTLRLCVOSTHYDRIRTLEDLNGTIGIYVPICSQKP 98

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Db      61 CDSTRLCQVSTHYDRTLEBDLMTGLGIYCPISQKP 98

RESULT 6
O778G9 HPV16 PRELIMINARY; PRT; 98 AA.
ID O778G9 HPV16
AC O778G9
DT 10-MAY-2005, integrated into UniProtKB/TREMBL.
DT 07-FEB-2006, entry version 1.
DT 07-FEB-2006, sequence version 3.
DE E7 protein (Fragment) .
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duijn M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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Cc      61 CDSTRLCQVSTHYDRTLEBDLMTGLGIYCPISQKP 98
Query Match          99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4,5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy      1 MHGGDTPLHEMYMDLOPETTDLYXXYXNDNSSEEDSIDGPAGOAEPBRAHNYIVTFCK 60
Db      1 MHGGTPTLHEMYMDLOPETTDLYCYEQUNDSSSEEDSIDGPAGOAEPBRAHNYIVTFCK 60
Oy      61 CDSTRLCQVSTHYDRTLEBDLMTGLGIYCPISQKP 98
Db      61 CDSTRLCQVSTHYDRTLEBDLMTGLGIYCPISQKP 98

RESULT 7
O778H1 HPV16 PRELIMINARY; PRT; 98 AA.
ID O778H1 HPV16
AC O778H1
DT 10-MAY-2005, integrated into UniProtKB/TREMBL.
DT 07-FEB-2006, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment) .
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duijn M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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DR	EMBL; AJ388065; CAB45123.1; -; Genomic_DNA.
DR	GO; GO:00055622; C:intracellular; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro; IPR000148; Papvi_E7.
DR	Pfam; PF00527; E7; 1.
DR	NON TER
FT	98
SQ	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
Query Match	99.0%; Score 512; DB 2; Length 98;
Best Local Similarity	96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	1 MHGDTPTLHEWMLDLPETTTDLYXXYXQLNDSSSEDEIDGPAGQAEPPRAHNYITPCKK 60 1 MHGDTPTLHEWMLDLPETTTDYCYEQANDSSEBDEIDGPAGQAEPPRAHNYITPCKK 60
Dd	1 MHGDTPTLHEWMLDLPETTTDYCYEQANDSSEBDEIDGPAGQAEPPRAHNYITPCKK 60
Oy	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPICSQKP 98 61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPICSQKP 98
Dd	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPICSQKP 98
RESULT 9	
ID	Q778H7_HPV16 PRELIMINARY; PRT; 98 AA.
AC	Q778H7; 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT	10-MAY-2005, integrated into UniProtKB/TrEMBL.
DI	10-MAY-2005, sequence version 1.
DT	07-FEB-2006, entry version 3.
DE	E7 protein (Fragment).
OS	Human papillomavirus type 16.
OC	Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
CC	Alphapapillomavirus.
OX	NCHI_Taxid=333760;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=20112892; PubMed=10644829;
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorthorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325(2000).
RL	J. Gen. Virol. 81:317-325(2000).
CC	-----
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CC	-----
DR	EMBL; AJ388064; CAB45121.1; -; Genomic_DNA.
DR	GO; GO:00055622; C:intracellular; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro; IPR000148; Papvi_E7.
DR	Pfam; PF00527; E7; 1.
DR	NON TER
FT	98
SQ	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
Query Match	99.0%; Score 512; DB 2; Length 98;
Best Local Similarity	96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	1 MHGDTPTLHEWMLDLPETTTDLYXXYXQLNDSSSEDEIDGPAGQAEPPRAHNYITPCKK 60 1 MHGDTPTLHEWMLDLPETTTDYCYEQANDSSEBDEIDGPAGQAEPPRAHNYITPCKK 60
Dd	1 MHGDTPTLHEWMLDLPETTTDYCYEQANDSSEBDEIDGPAGQAEPPRAHNYITPCKK 60
Oy	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPICSQKP 98 61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPICSQKP 98
Dd	61 CDSTLRCLCVOSTHVDIRTLEDLLMGTLGIYXPICSQKP 98

DT	10-MAY-2005, sequence version 1.
DT	07-FEB-2006, entry version 3.
DE	E7 protein (fragment).
OS	Human papillomavirus type 16.
OC	Virusae; dsDNA viruses, no RNA stage; Papillomaviridae;
CC	Alphapapillomavirus.
NCBI_TaxID=3333760;	
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=20112892; PubMed=10644829;
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT	"Analysis of human papillomavirus type 16 B6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol.	81:317-325(2000).
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
CC	EMBL; AJ388061; CAB45113.1; -; Genomic_DNA.
DR	GO; GO:0005622; C:intracellular; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro; IPR001481; Papv1_E7.
Pfam; PF00527; E7; 1.	
FT	NON TER
SQ	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
Query Match	99.0%; Score 512; DB 2; Length 98;
Best Local Similarity	96.9%; Pred. No. 4,5e-52;
Matches 95; Conservativity 0; Mismatches 3; Indels 0; Gaps 0;	
OY	1 MHGDPPTLAEWMLDLPETTTLYXXXYQLNDSESEDEIDGPAGGAEPDRAHNYVTFCCK 60 1 MHGDTPLHERMLDLQPETTDLVCYEQLDNDSSEDEIDGPAGGAEPDRAHNYVTFECK 60
Dd	61 CDSTLRLCVOSTHVADIRLTLEDLMGLTGIYPICSQKP 98 61 CDSTLRLCVOSTHVADIRLTLEDLMGLTGIYPICSQKP 98
Db	61 CDSTLRLCVOSTHVADIRLTLEDLMGLTGIYPICSQKP 98 61 CDSTLRLCVOSTHVADIRLTLEDLMGLTGIYPICSQKP 98
RESULT 10	
ID	Q778H9_HPV16 PRELIMINARY; PRT; 98 AA.
AC	Q778H9;
DT	10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT	10-MAY-2005, sequence version 1.
DE	07-FEB-2006, entry version 3.
DE	E7 protein (fragment).
OS	Human papillomavirus type 16.
OC	Virusae; dsDNA viruses, no RNA stage; Papillomaviridae;
CC	Alphapapillomavirus.
NCBI_TaxID=3333760;	
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=20112892; PubMed=10644829;
RA	van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT	"Analysis of human papillomavirus type 16 B6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol.	81:317-325(2000)
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
CC	EMBL; AJ388060; CAB45113.1; -; Genomic_DNA.
DR	GO; GO:0005622; C:intracellular; IEA.
DR	GO; GO:0003700; F:transcription factor activity; IEA.
DR	GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR	InterPro; IPR001481; Papv1_E7.
Pfam; PF00527; E7; 1.	
FT	NON TER
SQ	SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60
Db 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60

Qy 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPICSQKP 98
Db 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPICSQKP 98

RESULT 11
ID 077810 HPV16 PRELIMINARY; PRT; 98 AA.
AC 077810;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).

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CC EMBL; AJ388059; CAB4511.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60
Db 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60

Qy 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPICSQKP 98
Db 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPICSQKP 98

RESULT 12
ID 077811 HPV16 PRELIMINARY; PRT; 98 AA.
AC 077811;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).

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CC EMBL; AJ388058; CAB4510.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60
Db 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60

Qy 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPICSQKP 98
Db 61 CDSTLRCLCVOSTHVDIRLTEDLDMGTGIVPICSQKP 98

RESULT 13
ID 077813 HPV16 PRELIMINARY; PRT; 98 AA.
AC 077813;
DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
DT 10-MAY-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).

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CC EMBL; AJ388057; CAB4510.1; -; Genomic_DNA.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000148; Papv1_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
Best Local Similarity 96.9%; Pred. No. 4.5e-52;
Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60
Db 1 MHGDPPTLHEHYMLDLPETTTDLYXXQXNDSSSEDEIDGPAGQAEPPRAHNYITVFCCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSKP 98
 Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSKP 98

RESULT 14

077815 HPV16 PRELIMINARY; PRT; 98 AA.
 ID 077815 HPV16
 AC 077815;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 10-MAY-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE E7 protein (fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=333760;
 RN [1]

NUCLEOTIDE SEQUENCE

RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).

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 CC EMBL; AJ388056; CAB45105.1; -; Genomic_DNA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003780; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000148; Papv1_E7.
 DR Pfam; PF00527; E7; 1.
 DR NON TER 98
 FT NON TER 98

SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 99.0%; Score 512; DB 2; Length 98;
 Best Local Similarity 96.9%; Pred. No. 4.5e-52;
 Matches 95; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MHGDTPTLHEYMLDLPQETTDLYXXQUNDSSSEEDIDGPAGAEPPDRAHNYITVFCK 60
 Db 1 MHGDTPTLHEYMLDLPQETTDLYCYEQUNDSSSEEDIDGPAGAEPPDRAHNYITVFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSKP 98
 Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSKP 98

RESULT 15

077A11 HPV16 PRELIMINARY; PRT; 98 AA.
 ID 077A11 HPV16
 AC 077A11;
 DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE E7 protein (fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Alphapapillomavirus.
 OX NCBI_TaxID=333760;
 RN [1]

NUCLEOTIDE SEQUENCE

RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 RN [2]

RP NUCLEOTIDE SEQUENCE.

RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
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 CC EMBL; AJ242681; CAB45382.1; -; Genomic_DNA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR000148; Papv1_E7.
 DR Pfam; PF00527; E7; 1.
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SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;
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Qy 1 MHGDTPTLHEYMLDLPQETTDLYXXQUNDSSSEEDIDGPAGAEPPDRAHNYITVFCK 60
 Db 1 MHGDTPTLHEYMLDLPQETTDLYCYEQUNDSSSEEDIDGPAGAEPPDRAHNYITVFCK 60

Qy 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSKP 98
 Db 61 CDSTLRLCVOSTHVDIRTLIEDLIMGTIGIYXPICSKP 98

Search completed: June 6, 2006, 12:11:01
 Job time : 153.133 secs